TABLE 15: 169 GENES WITH SEQUENCE INFORMATION DEPICTED IN TABLE 16

Table 15 depicts UnigeneID, UnigeneTitle, Primekey, Predicted Cellular Localization, and Exemplar Accession for all of the sequences in Table 16. The information in Table 15 is linked by EosCode to Table 16.

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Unique Eos probeset identifier number

Pkey: ExAccn:

Exemplar Accession number, Genbank accession number

UnigenelD: 10 Unigene Title: Unigene number

EosCode:

Unigene gene title

Localization:

Internal Eos name
Predicted cellular localization of gene product

15	Pkey	ExAccn	UnigenelD	Unigene Title	EosCode	Localization
	100394	D84276	Hs.66052	CD38 antigen (p45)	PBC1	plasma membrane
		D87742	Hs.241552	KIAA0268 protein	PAB7	not determined
	101249	L33881	Hs.1904	protein kinase C, iota	OAA1	cytoplasmic
20	101485	M24736		selectin E (endothelial adhesion molecul	ACC5	plasma membrane
72 727	101514	M28214	Hs.123072	RAB3B, member RAS oncogene family	PFJ2	cytoplasmic
	101851	M94250	Hs.82045	midkine (neurite growth-promoting factor	LBH9	secreted
20 10 25 10	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	PDG3	
's_ }	102522	U53347	Hs.183556	solute carrier family 1 (neutral amino a	PFJ4	plasma membrane
25	102669	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	LEM9	cytoplasmic
1,11	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	LBG2	plasma membrane
£	103709	AA037316	Hs.13804	hypothetical protein dJ462O23.2	PDO6	•
2 22	104080	AA402971	Hs.57771	kallikrein 11	PBA6	secreted
	104144	AA447439	Hs.183390	hypothetical protein FLJ13590	PDM3	
30	104691	AA011176	Hs.37744	Homo sapiens beta-1 adrenergic receptor	PAV1	plasma membrane
₹		AA236476		transmembrane protein with EGF-like and		plasma membrane
				hypothetical protein MGC13170	PDO8	•
}_E		AA456135		ESTs	PAA4	plasma membrane
		AA609723		KIAA1344 protein	PAA3	not determined
35	107217	D51095		DKFZP586E1621 protein	PDG8	
3 5	108153	AA054237	Hs.40808	ESTs	PBF1	plasma membrane
	109014	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZII	NC	PDG7
				hypothetical protein FLJ13782	BCU4	not determined
	109890	H04649	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone F	ᆫ	PDG4
40	110151	H18836	Hs.31608	hypothetical protein FLJ20041	PAV9	plasma membrane
	112971	T17185	Hs.83883	transmembrane, prostate androgen induce	d	CHA1 not determined
	113021	T23855	Hs.129836	KIAA1028 protein	PDO3	
	114908	AA236545	Hs.54973	cadherin-like protein VR20	PFJ6	plasma membrane
	114965	AA250737	Hs.72472	ESTs	BCY2	mitochondrial
45	116393	AA599463		hypothetical protein MGC2648	PDV3	secreted
	116416	AA609219	Hs.39982	ESTs	OAB6	
	117698	N41002	Hs.45107	ESTs	PDT9	ER
	117984	N51919	Hs.106778	ATPase, Ca++ transporting, type 2C, mem	b	PAJ5 not determined
	118985	N94303		ESTs, Weakly similar to I54374 gene NF2		
50	119018	N95796	Hs.278695	Homo sapiens prostein mRNA, complete c	ds	PAB2 plasma membrane
	119126	R45175	Hs.117183	ESTs	PBF8	
	120992	AA398246	Hs.97594	KIAA1210 protein	PDG5	
	121710	AA419011		prostate androgen-regulated transcript 1	PDV5	
	121913	AA428062		ESTs; protease inhibitor 15 (PI15)	BCU7	vesicular
55	122041	AA431407	Hs.98732	Homo sapiens Chromosome 16 BAC clone	CIT	PAZ1 not determined
	122593	AA453310	Hs.128749	alpha-methylacyl-CoA racemase	PDO1	
	123209	AA489711	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN AL	.U S	PAA2 plasma membrane
		N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci		plasma membrane
		AA128075		transmembrane, prostate androgen induce		PDY4
60		Al167942		six transmembrane epithelial antigen of	PAA5	plasma membrane
		R38438		solute carrier family 15 (H+/peptide tra	PDO5	plasma membrane
			Hs.162859		PAA6	not determined
				secreted frizzled-related protein 4	BCX2	secreted
<i></i>				calcium/calmodulin-dependent protein kin		
65		W26769	Hs.109201	CGI-86 protein	PAV6	vesicular
	129389	AA621604		spondin 2, extracellular matrix protein	CJA5	not determined
				_		

		AA172056	11 44000	ESTs	PAB4	
		R73640	Hs.11260	hypothetical protein FLJ11264	PAJ3	secreted
		AA128997	Hs.18953	phosphodiesterase 9A	PEE6	nuclear
5		AA219134	HS.26691	ESTS	PBA7	
5		AA031360	Un 0100E	ESTs	PAA7	plasma membrane
		AA032221		six transmembrane epithelial antigen of	PM17	plasma membrane
		U81599	Hs.66731	homeo box B13	PFJ5	nuclear
		U42360	Hs.71119	Putative prostate cancer tumor suppresso		plasma membrane
10		X74331	Hs.74519	primase, polypeptide 2A (58kD)	PDM2	DDT4 miles also adulat
10		U07919	Hs.75746	aldehyde dehydrogenase 1 family, membe		PDT1 mitochondrial
		U07919	Hs.75746	aldehyde dehydrogenase 1 family, membe		PDT1 mitochondrial
		AA045870	Hs.79136	Homo sapiens mRNA; cDNA DKFZp564A0	. *	PAB9 cytoplasmic
		U41060		LIV-1 protein, estrogen regulated	BCR4	plasma membrane
15		A1800004		hypothetical protein	PEU4	nuclear
13		AI869666		MAD (mothers against decapentaplegic, D		cytoplasmic
				relaxin 1 (H1) ESTs, Weakly similar to Homolog of rat Z	PBH3	secreted
		D30891	Hs.19525	hypothetical protein FLJ22794	PBM4	not determined
		AW503733		KIAA1488 protein	PBY3	not determined
20		Al460004	Hs.31608	hypothetical protein FLJ20041	PEU5	plasma membrane
20		AI734009		KIAA1603 protein	PCQ8	plasma memorane
		Al420227		ESTs, Weakly similar to A46010 X-linked	PBH1	plasma membrane
			Hs.156142		PEN3	plasma membrane
, pol.		Al338013	Hs.140546		PCW3	plasma memorane
25		Al973051	Hs.224965		PET5	
·II		Al682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	PBH8	
4.1			Hs.120591		PBY2	
2 5		Al732100	Hs.187619		PBY1	
411 			Hs.136319		BFF8	not determined
30		Al538226	Hs.32976	guanine nucleotide binding protein 4	CBO7	cytoplasmic
	314907	Al672225	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TI	RICH	PBM2not determined
ij	315051	AW292425		ESTs	PBM9	
***			Hs.134427		PBJ7	plasma membrane
2.5			Hs.153023		PBJ9	
35		Al654187	Hs.195704		PBQ6	
				deoxyribonuclease II beta	PBQ7	
3 2			HS.159066	hypothetical protein FLJ10188	PBJ1	cytoplasmic
		AF071538 AA460775	He cook	prostate epithelium-specific Ets transcr	PEN1	
40				ESTs, Weakly similar to T17248 hypotheti ATP-binding cassette, sub-family C (CFTR		plasma membrane
			3Hs.159330		PEL9	plasma membrane
		AF038966		secretory carrier membrane protein 1	PBY4	not determined
ļui.				Homo sapiens LUCA-15 protein mRNA, sp		PBY8 not determined
		W07459	Hs.157601		CBF9	secreted
45				Homo sapiens cDNA FLJ12166 fis, clone N		PBQ1 not determined
			Hs.293616		PCQ7	plasma membrane
		AF055019		Homo sapiens clone 24670 mRNA sequen		PCI2 not determined
	323287	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAI	NS	PBJ5
	324295	Al146686	Hs.143691	ESTs	PBQ9	not determined
50	324430	AA464018	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone	C	PBY6 not determined
	324603		Hs.292934		PBM3	
			Hs.195839	ESTs, Weakly similar to I38022 hypotheti		cytoplasmic
		Al685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapi		PCW6
<i></i>		Al694767		Homo sapiens cDNA FLJ13581 fis, clone F		PBJ4 plasma membrane
55		Al557019	Hs.116467	small nuclear protein PRAC	CBK1	nuclear
	330211	1101000			PBJ2	not determined
	330546			guanine nucleotide binding protein 4	PEW1	cytoplasmic
		AA449677	Hs.15251	hypothetical protein	PBM1	not determined
60	330790			TMPRSS2, transmembrane protease, serin		PEL3 plasma membrane
00	331099		Hs.91202	ESTS	PBQ4	plasma membrane
	331490		Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D0	•	PCQ1cytoplasmic
		AA431407	Hs.291039	ESTs, Moderately similar to T14342 NSD1	PCI4	nuclear not determined
	332247		110.30002	gb:za21f09.s1 Soares fetal liver spleen	PBQ5	not determined nuclear
65		AA340504		gb:hw31a09.x1 NCI_CGAP_Kid11 Homo s		PBJ8 not determined
0.5	332697			transgelin 2	PBQ8	secreted
	332798	. 0-000		nanogomi z	PBH2	nuclear
	334447				PBY9	not determined
	338255				PBY7	not determined

	401424				PFG2	mitochondrial
	407122	H20276	Hs.31742	ESTs	PEW7	
	408430		Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	PEZ3	plasma membrane
		AF216077		Homo sapiens clone HB-2 mRNA sequence		PEY1
5		AK000631		hypothetical protein FLJ20624	PFG1	nuclear
5		NM_005982		sine oculis homeobox (Drosophila) homolo		nuclear
		U80034	Hs.68583	mitochondrial intermediate peptidase	PEZ9	mitochondrial
		BE244589		, ,	PFJ3	cytoplasmic
				glyoxalase I	OBH6	cytopiasmic
10			Hs.246973		PFC6	
10				Homeo box A13	PEZ5	
			Hs.130853			secreted
	417153		Hs.81343	"collagen, type II, alpha 1 (primary ost	PFJ1	
		AA279490		calmegin	PFA1	ER
15		Al820961	Hs.193465		PEY4	
13		NM_004996		ATP-binding cassette, sub-family C (CFTR		
		U24577	Hs.93304	"phospholipase A2, group VII (platelet-a	PFH9	secreted
					PFH2	plasma membrane
		_		"arachidonate 15-lipoxygenase, second ty		cytoplasmic
20		AW102723		guanylate cyclase 1, soluble, alpha 3	PFA3	
20			9Hs.154424	"deiodinase, iodothyronine, type II"	PFH6	secreted
		AF030880		solute carrier family, member 4	PFD4	plasma membrane
the seed.		AA418000		potassium intermediate/small conductance		plasma membrane
				KIAA0575 gene product	PFD6	nuclear
		AA460421		ESTs	PEZ7	
25			Hs.119383		PEY5	
is a		BE245562		adrenergic, beta-2-, receptor, surface	PEZ4	plasma membrane
7-4		-		Rho GTPase activating protein 6	PFG6	nuclear
SEE		D89053		fatty-acid-Coenzyme A ligase, long-chain	PEZ1	
30		NM_002742	2Hs.2891	protein kinase C, mu	PFH4	cytoplasmic
϶υ		AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sap		PFA2
		Al669973	Hs.200574		PEW8	
fi		W07088	Hs.293685		PFG3	
			Hs.325198		PEY3	
£ 25		Al446444		ESTs, Weakly similar to B28096 line-1 pr	PEW5	
35		Al972867	Hs.7130	copine IV	PEW6	
			Hs.128612		PFC8	
is mil		AB028945		cortactin SH3 domain-binding protein	PEZ6	
11		AF126245	Hs.14791	"acyl-Coenzyme A dehydrogenase family, i		PFH7
540		AF035269		phosphatidylserine-specific phospholipas	PFH8	
40						
*F 2227		NM_01425		odz (odd Oz/ten-m, Drosophila) homolog 1		plasma membrane
l-i		AF055575		calcium channel, voltage-dependent, L ty		plasma membrane
		U80456	Hs.27311	single-minded (Drosophila) homolog 2	PFJ8	
15	451982		Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1		PFG9plasma membrane
45		Al922988		ESTs	PFD8	
		NM_00220		ISL1 transcription factor, LIM/homeodoma		nuclear
				hypothetical protein FLJ21062	PFC5	cytoplasmic
	452946	X95425	Hs.31092	EphA5	PFH3	plasma membrane

TABLE 15A shows the accession numbers for those primekeys lacking a unigeneID in Table 15. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

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Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkev CAT number Accession

	Pkey	CAT number	Accession
	116393	131543_1	Al972402 Al634409 Al523716 Al799749 W44518 Al424438 Al688513 Al971048 Al686324 AW013854 AA588483 AA528111 Al627428
20			AI582200 AI669296 AI826926 AI620526 AI669958 AI972458 AI924500 AA512903 W44517 AA35363 AW238997 BE300165
"D			BE250665 AA284195 AA523420 W52834 Al471970 Al952824 AW003820 AW009463 AA669796 AA114966 Al653342 AA115038
1.4			AI342150 AI092100 AI968211 W51994 AI804005 AI201420 AI123210 AI738405 AI674964 AI970341 AW027500 AI493316 AI333193
177			AI139353 AA599463 AI656163 AI804200 AI365321 AI990213 AI657011 AA650025 AI968810 AI341978 AA599839 AW592602
25	404405	10110 1	AA644289 Al468578 Al565265 Al565228 BE221535 AW973052
<u>25</u>	101485	18113_1	AA296520 AL021940 M30640 NM_000450 M24736 M61894 AL047443 H39560 Al694691 AA916787 Al214796 AA939085 Al150616 AA412553 AA412545 Al051015 T27654 AA694430
	126200	17331_1	AA088767 AF224278 AA128075 AL035541 AA027926 AI761441 AI972096 AW071693 AI742327 AI377498 AI804815 AI640802
12	120399	1/331_1	ANDOS/10/ AF224276 AA126075 ALCGGG41 AND27320 A1761441 A1572950 AWO/1050 A1742027 A1577450 A1004010 A1040002 A1885001 A1921394 AA595115 N71820 A1921217 AWO07283 A1467828 A1369306 AA917446 A1493698 AA088701 AA126899 A1936228
100			AW204238 Al039567 Al925027 BE138909 AW452945 AW135998 AA310984 AA027860 AW073519 Al537597 AA953976 Al521341
30			AW273569 AW050740 AA536113 AA559064 AI474392 AW135709 AA535181 AW572959 AA570597 AI905464 AI677810 AI587642
130			AW975102 AA424310 AA482527 N64192 AA658276 AW889117 AA486591 AW889172 Al381990 Al381991 Al673419 Al990950
****			AA487031 Al272934 Al150565 AA229168 AW316722 Al142707 BE222396 AA614168 AA122026 AW338227 AA632457 Al968726
			AW369662 AA512956 AA541675 AA451748 Al250993 BE146418 AA122025
	132964	94346 1	Al362575 Al805082 AW263421 Al432462 AA135870 AA031360 AA031604 AA298475 AA298464
3 5		21074 1	NM 012445 AB027466 BE407510 BE047605 AA047125 AW084003 AA149494 AA149490 AA292528 AA570505 AA526186 AW006250
Ū			AW007762 Al341557 Al799666 Al972710 Al377966 Al962810 Al084783 Al458032 Al190971 AW148913 AA372354 AW970032
			AW007426 AA650188 Al123203 Al122890 Al280975 W73595 W73495 Al863238 AA374109 AA603986 AW149089 AW957523
).L			Al307748 Al921067 Al336463 F24537 Al380460 Al367500 Al189309 Al814701 Al766921 AW572106 AA037024 AW072576 AA578293
			Al288103 AA235464 AW450642 AA574230 AW294024 Al589229 Al580733 AW512227 AA877009 Al660255 AW188597 AA558228
40			Al572782 AA658397 Al274628 Al866359 AA864573 Al264439 AA621604 AW515493 AW243333 Z39737 Al567038 AA573997
			AA573559 AW236431 Al652870 Al684973 AA034505 AA047126
		156454_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	107217	9836_1	AL080235 AA031750 D81382 Al480231 Al095947 Al560953 BE010721 Al870290 AA374945 AA125792 D51527 D51556 Al685541
45			D51559 AW117286 AA195741 Al675138 AW593439 Al201885 T30590 AW952100 D51095 AA523864 W70043 AA987586 Al421515
45	101710	10000 1	Al205532 AA127069 Al337367 D51595 Al453785 AW075677 AW088359 C14287 C14284
	121710	19266_1	AF163474 NM_016590 AF163475 AI761105 AI770098 AA410580 AA411616 AI590343 AI739050 AL050198 AI862645 AA419104
			AA513809 AA333032 Al816915 AW139625 AA640889 Al311391 Al627693 AW135514 AA419011 Al269149 Al245259 Al970008
	404040	001015 1	A1970017 AW139445 AA569503 A1761072 A1766179 A1759995 A1300776 A1870129 AW150770 AA226501 AA226220
50	121913	291015_1	Al249368 Al742316 AA428062 AA442089 Al864189 BE349478 Al803475 Al584049 BE552085 Al088609 Al264197 Al886144 Al129474 Al307145 BE181300 AW058403 Al696838 AW748598 AA442196 Al216428
50	102208	entrez U4235	
		347217 1	AW292425 BE467167 AI702953 BE550961 BE222309 AI299348 AI693336 AA541708
		336411 1	Al685464 AW971336 AA513587 AA525142
		16065 1	NM 012391 AF071538 AB031549 Al685592 Al745526 AA662204 AW130657 AA662164 AW971121 Al668916 AA513274 Al991223
55			Al979170 AW298436 AA639821 Al859010 AW513942 Al687669 AA662521 AA548598 Al345056 Al305374 BE043418 Al432856
			Al334840 Al379796 Al492693 Al307915 BE042082 Al307834 Al307858 Al309488 BE042210 Al435670 Al371605 Al862491 Al284563
			Al306872 Al255044 Al254601 Al251236 Al473073 Al473042 Al432760 Al435664 Al336826 Al289365 Al369096 Al862274 Al334871
			Al349863 Al250405 Al377617 Al309895 Al313017 Al862291 Al311936 Al378718 Al305722 Al306769 Al308888 Al334565 Al862296
			Al344230 Al435685 Al344087 Al378696 Al311209 Al435775 Al310611 Al311154 Al432289 Al431561 Al492681 Al432867 Al335288
60			Al492796 Al432769 Al310299 Al432273 Al379820 Al275319 Al435753 Al609441 Al432767 Al369100 Al311420 Al349974 Al247157
			Al334677 Al270910 Al224320 Al305608 Al334489 Al377152 Al350012 Al370086 Al335053 Al306781 Al306750 Al334849 Al334874
			Al340380 Al307876 Al305974 Al305972 Al311521 Al334872 Al862509 Al311498 Al335051 Al289684 Al310859 Al311862 Al862483
			Al492775 Al307906 Al492708 Al289693 Al340373 Al307910 Al311359 Al435653 Al334865 Al311492 Al492809 Al492690 Al431576
65			Al862268 Al311879 Al308435 Al492792 Al862512 Al275321 Al431568 Al431564 Al307885 Al307926 Al435692 Al435778 Al310182
03			Al308894 Al492707 Al492713 Al308560 Al307829 Al343234 Al580598 AW472796 Al340918 Al310243 Al309368 Al307920 Al289665

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10

15

TABLE 15B shows the genomic positioning for those primekeys lacking unigene ID's and accession numbers in Table 15. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Ref:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA

sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted. Strand: Indicates nucleotide positions of predicted exons. Nt_position:

Pkey	Ref	Strand	Nt_position
334447	Dunham, I. et.al.	Plus	14308764-14308824
332798	Dunham, I. et.al.	Minus	232147-231974
338255	Dunham, I. et.al.	Minus	15242294-15242231
330211	6013592	Plus	59158-59215
401424	8176894	Plus	24223-24428

TABLE 11 AND SEQUENCE LISTING

SEQ ID NO:1 BCU4 DNA SEQUENCE



GCGAAACACT CCAAAGAGAT AGGAAAACTT GCCGCCTCTT CTTTTTTGTC CCTTAATCAA 4380 ACTCAAATAA GCTTAAAAAA AATCCATGGA AGATCATGGA CATGTGAAAT GAGCATTTTT 4440 5 TTCTTTTCTT TTTTTTTTT TTTTTTAAC AAAGTCTGAA CTGAACAGAA CAAGACTTTT 4500 TCCTCATACA TCTCCAAATT GTTTAAACTT ACTTTATGAG TGTTTGTTTA GAAGTTCGGA 4560 CCAACAGAAA AATGCAGTCA GATGTCATCT TGGAATTGGT TTCTAAAAGA GTAAGGCATG 4620 TCCCTGCCCA GAAACTTAGG AAGCATGAAA TAAATCAAAT GTTTATTTTC CTTCTTATTT 4680 AAAATCATGC TAATGCAACA GAAATAGAGG GTTTGTGCCA AATGCTATGA ACGGCCCTTT 4740 10 CTTAAAGACA AGCAAGGGAG ATTGATATAT GTACAATTTG CTCTCATGTT TTT SEQ ID NO:2 BCU4 Protein sequence: NP 079191.1 Protein Accession #1 15 31 MSQESDNNKR LVALVPMPSD PPFNTRRAYT SEDEAWKSYL ENPLTAATKA MMIINGDEDS 60 AAALGLLYDY YKVPRDKRLL SVSKASDSQE DQEKRNCLGT SEAQSNLSGG ENRVQVLKTV 120 20 PVNLSLNQDH LENSKREQYS ISFPESSAII PVSGITVVKA EDFTPVFMAP PVHYPRGDGE 180 EQRVVIFEQT QYDVPSLATH SAYLKDDQRS TPDSTYSESF KDAATEKFRS ASVGAEEYMY 240 DQTSSGTFQY TLEATKSLRQ KQGEGPMTYL NKGQFYAITL SETGDNKCFR HPISKVRSVV 300 MYVFSEDKNR DEOLKYWKYW HSROHTAKOR VLDIADYKES FNTIGNIEEI AYNAVSFTWD 360 VNEEAKIFIT VNCLSTDFSS QKGVKGLPLM IQIDTYSYNN RSNKPIHRAY CQIKVFCDKG 420 25 30 35 AERKIRDEEQ KQNRKNGKGQ ASQTQCNSSS DGKLAAIPLQ KKSDITYFKT MPDLHSQPVL 480 FIPDVHFANL QRTGQVYYNT DDEREGGSVL VKRMFRPMEE EFGPVPSKQM KEEGTKRVLL 540 YVRKETDDVF DALMLKSPTV MGLMEAISEK YGLPVEKIAK LYKKSKKGIL VNMDDNIIEH 600 YSNEDTFILN MESMVEGFKV TLMEI SEQ ID NO:3 BCU7 DNA SEQUENCE VARIANT 1: AA428062 Nucleic Acid Accession #: 1-777 (entire sequence represents open reading frame) Coding sequence: 11 21 31 41 51 ÍÕ ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCCTGTTCT CCCTTCTCTG TGAAGCAAGT 60 ACCGTCGTCC TACTCAATTC CACTGACTCA TCCCCGCCAA CCAATAATTT CACTGATATT 120 40 GAAGCAGCTC TGAAAGCACA ATTAGATTCA GCGGATATCC CCAAAGCCAG GCGGAAGCGC 180 TACATTTCGC AGAATGACAT GATCGCCATT CTTGATTATC ATAATCAAGT TCGGGGCAAA 240 I GTGTTCCCAC CGGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300 GCAGAGGCTT GGGCGGCTAC TTGCATTTGG GACCATGGAC CTTCTTACTT ACTGAGATTT 360 į TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATTCTCCA GTTGGTCAAG 420 45 CCATGGTATG ATGAAGTGAA AGATTATGCT TTTCCATATC CCCAGGATTG CAACCCCAGA TGTCCTATGA GATGTTTTGG TCCCATGTGC ACACATTATA CGCAGATGGT TTGGGCCACT 540 TCCAATCGGA TAGGATGCGC AATTCATGCT TGCCAAAACA TGAATGTTTG GGGATCTGTG 600 TGGCGACGTG CAGTTTACTT GGTATGCAAC TATGCCCCAA AGGGCAATTG GATTGGAGAA 660 il da GCACCATATA AAGTAGGGGT ACCATGTTCA TCTTGTCCTC CAAGTTATGG GGGATCTTGT 720 50 ACTGACAATC TGTGTTTTCC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA SEQ ID NO:4 BCU7 DNA SEQUENCE VARIANT 2: Nucleic Acid Accession #: AA428062 Coding sequence: 1-777 (entire sequence represents open reading frame) 55 11 21 31 41 51 60 ATGATAGCAA TCTCTGCCGT CAGCAGTGCA CTCCTGTTCT CCCTTCTCTG TGAAGCAAGT 60 ACCGTCGTCC TACTCAATTC CACTGACTCA TCCCCGCCAA CCAATAATTT CACTGATATT 120 GAAGCAGCTC TGAAAGCACA ATTAGATTCA GCGGATATCC CCAAAGCCAG GCGGAAGCGC TACATTTCGC AGAATGACAT GATCGCCATT CTTGATTATC ATAATCAAGT TCGGGGCAAA GTGTTCCCAC CGGCAGCAAA TATGGAATAT ATGGTTTGGG ATGAAAATCT TGCAAAATCG 300 65 GCAGAGGCTT GGGCGGCTAC TTGCATTTGG GACCATGGAC CTTCTTACTT ACTGAGATTT 360 TTGGGCCAAA ATCTATCTGT ACGCACTGGA AGATATCGCT CTATTCTCCA GTTGGTCAAG 420 CCATGGTATG ATGAAGTGAA AGATTATGCT TTTCCATATC CCCAGGATTG CAACCCCAGA 480 TGTCCTATGA GATGTTTTGG TCCCATGTGC ACACATTATA CGCAGATGGT TTGGGCCACT 540 TCCAATCGGA TAGGATGCGC AATTCATACT TGCCAAAACA TGAATGTTTG GGGATCTGTG 600 70 TGGCGACGTG CAGTTTACTT GGTATGCAAC TATGCCCCAA AGGGCAATTG GATTGGAGAA 660 GCACCATATA AAGTAGGGGT ACCATGTTCA TCTTGTCCTC CAAGTTATGG GGGATCTTGT 720 ACTGACAATC TGTGTTTTCC AGGAGTTACG TCAAACTACC TGTACTGGTT TAAATAA SEQ ID NO:5 BCU7 Protein sequence Variant 1: 75 Protein Accession #: 21 31 41 51 MIAISAVSSA LLFSLLCEAS TVVLLNSTDS SPPTNNFTDI EAALKAQLDS ADIPKARRKR

TGGTGCCAAG TGCCACATCC CTTCCGATCC ATTCCCCTCT GTATCCTCGG AGCACCCCAG 4260 TTTGCCTTTG ATGTGTCCGC TGTGTATGTT AGCTGAACTT TGATGAGCAA AATTTCCTGA 4320



YEELVDVNCS AVLRFFFCAM YAPICTLEFL HDPIKPCKSV CQRARDDCEP LMKMYNHSWP 120 ESLACDELPV YDRGVCISPE AIVTDLPEDV KWIDITPDMM VQERPLDVDC KRLSPDRCKC 180 KKVKPTLATY LSKNYSYVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTQVPLITN 240 SSCQCPHILP HQDVLIMCYE WRSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300 KKKTAGRTSR SNPPKPKGKP PAPKPASPKK NIKTRSAQKR TNPKRV

5

SEQ ID NO:9 CBK1 DNA SEQUENCE Nucleic Acid Accession #: NM_032391 10 129-302 (underlined sequences correspond to start and stop codons) Coding sequence: 11 51 15 GTCCTTCCTC TCCTAGCCTA AGGCGTGCAA ACAGAGCGCC ACTGGGAGGC TGAAACCTTT AGGCCGATGC TTGCTTGCAA GGTCAGGCAA GCTGGATTCT GGTCCCCACC TTTGCAGAGA 120 GAACAGCGAT GTTGTGCGCC CATTTCTCAG ATCAAGGACC GGCCCATCTT ACTACCTCCA 180 AGAGTGCTTT TCTCTCTAAT AAGAAAACAT CTACTTTGAA ACATCTACTG GGCGAGACCA 240 GGAGTGATGG CTCAGCCTGT AATTCTGGAA TTTCGGGAGG CCGAGGCAGG AAGATTCCTT 300 20 GAGCACAGGA GTTCCAGACC AGCCTGGGCA ATGTAGCAAG ACGCTGTCTC TATTTATACA 360 ATAAAATTTT TTTAAAAAAG G SEQ ID NO:10 CBK1 Protein sequence:
Protein Accession #: NP_115767 25 30 35 21 31 41 51 11 MLCAHFSDQG PAHLTTSKSA FLSNKKTSTL KHLLGETRSD GSACNSGISG GRGRKIP SEQ ID NO:11 CHA1 DNA SEQUENCE Nucleic Acid Accession #: NM_020182 Coding sequence: 96-854 (underlined sequences correspond to start and stop codons) 51 11 21 31 41 40 45 TCCTTGGGTT CGGGTGAAAG CGCCTGGGGG TTCGTGGCCA TGATCCCCGA GCTGCTGGAG AACTGAAGGC GGACAGTCTC CTGCGAAACC AGGCAATGGC GGAGCTGGAG TTTGTTCAGA 120 TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCACGTGC CTGCTGAGCC 180 ACTACAAGCT GTCTGCACGG TCCTTCATCA GCCGGCACAG CCAGGGGGGG AGGAGAAGA 240 ATGCCCTGTC CTCAGAAGGA TGCCTGTGGC CCTCGGAGAG CACAGTGTCA GGCAACGGAA TCCCAGAGCC GCAGGTCTAC GCCCGCCTC GGCCCACCGA CCGCCTGGCC GTGCCGCCCT 300 360 TCGCCCAGCG GGAGCGCTTC CACCGCTTCC AGCCCACCTA TCCGTACCTG CAGCACGAGA TCGACCTGCC ACCCACCATC TCGCTGTCAG ACGGGGAGGA GCCCCCACCC TACCAGGGCC 480 CCTGCACCCT CCAGCTTCGG GACCCCGAGC AGCAGCTGGA ACTGAACCGG GAGTCGGTGC 540 GCGCACCCC AAACAGAACC ATCTTCGACA GTGACCTGAT GGATAGTGCC AGGCTGGGCG 600 50 660 GCCCCTGCCC CCCCAGCAGT AACTCGGGCA TCAGCGCCAC GTGCTACGGC AGCGGCGGGC GCATGGAGGG GCCGCCGCCC ACCTACAGCG AGGTCATCGG CCACTACCCG GGGTCCTCCT 720 TCCAGCACCA GCAGAGCAGT GGGCCGCCCT CCTTGCTGGA GGGGACCCGG CTCCACCACA 780 CACACATCGC GCCCCTAGAG AGCGCAGCCA TCTGGAGCAA AGAGAAGGAT AAACAGAAAG 840 GACACCCTCT CTAGGGTCCC CAGGGGGGCC GGGCTGGGGC TGCGTAGGTG AAAAGGCAGA 900 55 ACACTCCGCG CTTCTTAGAA GAGGAGTGAG AGGAAGGCGG GGGGCGCAGC AACGCATCGT 960 GTGGCCCTCC CCTCCCACCT CCCTGTGTAT AAATATTTAC ATGTGATGTC TGGTCTGAAT 1140 60 SEQ ID NO:12 CHA1 Protein sequence: Protein Accession #: NP 064567 65 31 41 21 11 MAELEFVQII IIVVVMMVMV VVITCLLSHY KLSARSFISR HSQGRRREDA LSSEGCLWPS 60 ESTYSGNGIP EPQYYAPPRP TDRLAVPPFA QRERFHRFQP TYPYLQHEID LPPTISLSDG EEPPPYQGPC TLQLRDPEQQ LELNRESVRA PPNRTIFDSD LMDSARLGGP CPPSSNSGIS ATCYGSGGRM EGPPPTYSEV IGHYPGSSFQ HQQSSGPPSL LEGTRLHHTH IAPLESAAIW 120 70 SKEKDKOKGH PL SEQ ID NO:13 CJA5 DNA SEQUENCE 75 Nucleic Acid Accession #: NM_012445 276-1271 (underlined sequences correspond to start and stop codons) Coding sequence: 11 31 41 51 80 305

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SEQ ID NO:17 LEM9 DNA SEQUENCE

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SEQ ID NO:23 PAA2 DNA SEQUENCE

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	ACTITIVECCE A CCA	בכככיייייכי ככ	ግጥር ር ልጥር ጥር	TTCCATTGTG	ACTTCTCTGA	TAAAGCGTCT .	1380
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	መመመረጥር አጥርር ጥርጥ	ነል ግጥፈልግጋል፣	ጥውጥርርጥጥጥ	ATCTTTTCAA	AGCTCTTTTA	ATAGGATTTT	1500
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	AACACAGGTA AAA TCATGGAAGT CTT	ATGCACC T	PTTAAAGCA	CTACGTTTTC	ACAGACAATA	TACGTTCGTA	1680
	መመጥ አጥር ጥልርጥ ጥጥር	AGGGAAG G	TCTAATAAA	AAGACAAGCG	GTGGGACAGA	GGGAACCTAC	1740
.s.==.	አአርሮአአአአልሮ ጥርር	የርጥልርኔጥር ጥ	PTGCAGTTA	TGTGCTTTAT	GCCACGAAGA	ACTGAAGTAT	1800
= 25	CONCOUNT TOTAL	יא האמממתיי	PTCATATGG	AACTGAGTTC	CCAGCATCAT	CTTATTCTGA	1860
Total Control	ATAGCATTCA GT	ATTAAGA A	TACAATTT	TAACCTTCAT	GTAGCTAAGT	AAGAGAGTAA	1920 1980
phone phone	AAGGGTTTCA AGA CAACTGCACT AGG	AGCTTTGT AC	CAGTCTCGA	TGGCCCACAC	AAGACGCTGTT	ACTTCCCTTT	2040
diam'	CAACCAAAAC TTT	የተተልርጥርጥ ርና	TATTGTACA	TAAAGTCGGC	TTCTCTAAAG	AACCATTGGT	2100
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il a il il il	TOTO COTTO AC CA	COPTOTA T	CTGTGACAG	TAAGCCCTCC	TGGGATGTCT	GTGCCATGTG	3180
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                                                                                      1500
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                                                                                      1560
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           GTTAGAGGAC TGCCTGTGAT CCTGGCCACT AGGCCAAGAG GCCCTATGAA GGTGGCGGGA
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           REKNFAKGSE EQGRVLMNLQ NNEAGRRAVY KMADVACKCH GVSGSCSLKT CWLQLAEFRK
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	MOCOL EDITO	TOWANOCIANA	(D. MICHEL CTC	D DOCTOTICE		F TEL OCOPET	
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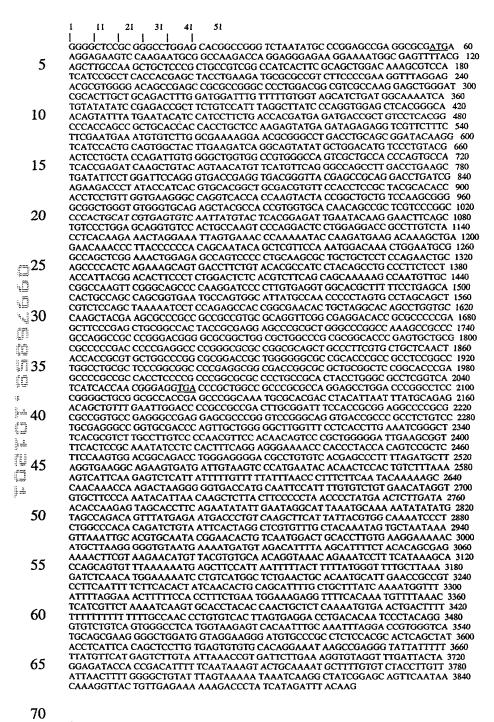
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5 SEQ ID NO:114 PFJ6 Protein sequence:
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Nucleic Acid Accession #: NM_006361
Coding sequence: NM_006361
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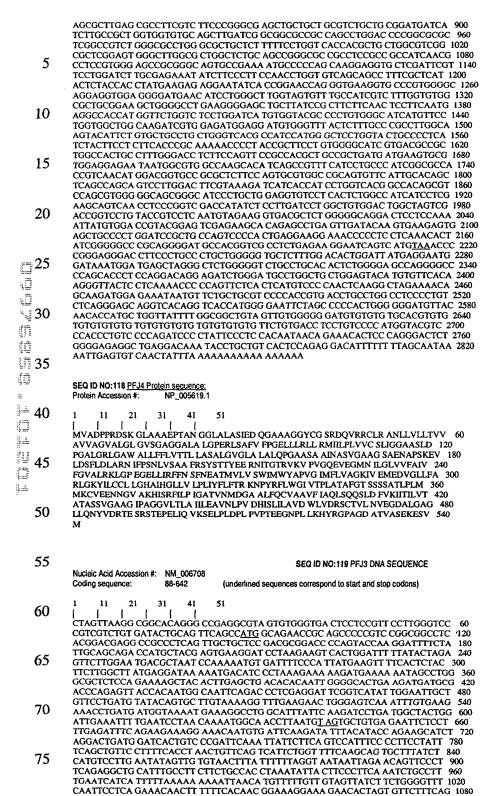
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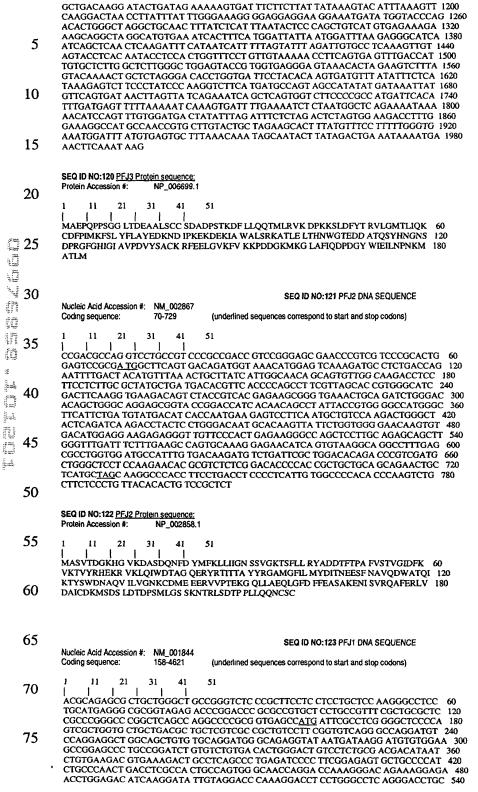
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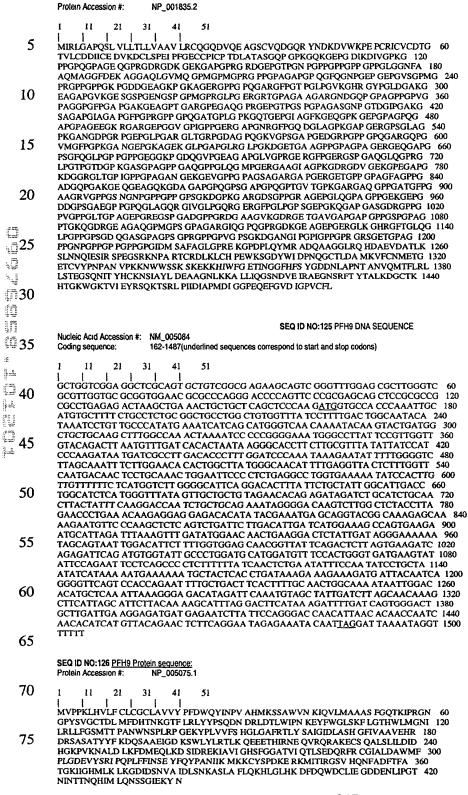
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GGGTGAGAGT GGTTCCCCGG GTGAGAACGG ATCTCCGGGC CCAATGGGTC CTCGTGGCCT 1140
GCCTGGTGAA AGAGGACGGA CTGGCCCTGC TGGCGCTGCG GGTGCCCGAG GCAACGATGG 1200 10 TCAGCCAGGC CCCGCAGGTC CTCCGGGTCC TGTCGGTCCT GCTGGTGGTC CTGGCTTCCC 1260 TGGTGCTCCT GGAGCCAAGG GTGAAGCCGG CCCCACTGGT GCCCGTGGTC CTGAAGGTGC 1320 TCAAGGTCCT CGCGGTGAAC CTGGTACTCC TGGGTCCCCT GGGCCTGCTG GTGCCTCCGG 1380 15 TAACCCTGGA ACAGATGGAA TTCCTGGAGC CAAAGGATCT GCTGGTGCTC CTGGCATTGC 1440 TGGTGCTCCT GGCTTCCCTG GGCCACGGGG TCCTCCTGGC CCTCAAGGTG CAACTGGTCC 1500 TCTGGGCCCG AAAGGTCAGA CGGGTGAACC TGGTATTGCT GGCTTCAAAG GTGAACAAGG 1560 CCCCAAGGGA GAACCTGGCC CTGCTGGCCC CCAGGGAGCC CCTGGACCCG CTGGTGAAGA 1620 AGGCAAGAGA GGTGCCCGTG GAGAGCCTGG TGGCGTTGGG CCCATCGGTC CCCCTGGAGA 1680 20 AAGAGGTGCT CCCGGAAACC GCGGTTTCCC AGGTCAAGAT GGTCTGGCAG GTCCCAAGGG 1740 AGCCCCTGGA GAGCGAGGGC CCAGTGGTCT TGCTGGCCCC AAGGGAGCCA ACGGTGACCC 1800 TGGCCGTCCT GGAGAACCTG GCCTTCCTGG AGCCCGGGGT CTCACTGGCC GCCCTGGTGA 1860 TGCTGGTCCT CAAGGCAAAG TTGGCCCTTC TGGAGCCCCT GGTGAAGATG GTCGTCCTGG 1920 ACCTCCAGGT CCTCAGGGGG CTCGTGGGCA GCCTGGTGTC ATGGGTTTCC CTGGCCCCAA 1980 AGGTGCCAAC GGTGAGCCTG GCAAAGCTGG TGAGAAGGGA CTGCCTGGTG CTCCTGGTCT 2040 GAGGGGTCTT CCTGGCAAAG ATGGTGAGAC AGGTGCTGCA GGACCCCCTG GCCCTGCTGG 2100 ACCTGCTGGT GAACGAGGCG AGCAGGGTGC TCCTGGGCCA TCTGGGTTCC AGGGACTTCC 2160 TGGCCCTCCT GGTCCCCCAG GTGAAGGTGG AAAACCAGGT GACCAGGGTG TTCCCGGTGA 2220 AGCTGGAGCC CCTGGCCTCG TGGGTCCCAG GGGTGAACGA GGTTTCCCAG GTGAACGTGG 2280 CTCTCCCGGT GCCCAGGGCC TCCAGGGTCC CCGTGGCCTC CCCGGCACTC CTGGCACTGA 2340 TGGTCCCAAA GGTGCATCTG GCCCAGCAGG CCCCCTGGC GCACAGGGCC CTCCAGGTCT 2400 TCAGGGAATG CCTGGCGAGA GGGGAGCAGC TGGTATCGCT GGGCCCAAAG GCGACAGGGG 2460
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5 Nucleic Acid Accession #: NM 015900 32-1402 (underlined sequences correspond to start and stop codons) Coding sequence: 10 CACGAGCGC ACGAGGATTT CCAGCTCAGC GATGCCCCCA GGTCCCTGGG AGAGCTGCTT 60 CTGGGTGGGG GGCCTCATTT TGTGGCTCAG CGTTGGAAGT TCAGGGGATG CACCTCCTAC 120 CCCACAGCCA AAGTGCGCTG ACTTCCAGAG CGCCAACCTT TTTGAAGGCA CCGATCTCAA 180 AGTCCAGTTT CTCCTCTTTG TCCCTTCGAA TCCTAGCTGT GGGCAGCTAG TAGAAGGAAG 240 CAGTGACCTC CAAAACTCTG GGTTCAATGC CACTCTGGGA ACCAAACTAA TTATCCATGG 300 15 ATTCAGGGTT TTAGGAACAA AGCCTTCCTG GATTGACACA TTTATTAGAA CCCTTCTGCG 360 TGCAACGAAT GCTAATGTGA TTGCCGTGGA CTGGATTTAT GGGTCTACAG GAGTCTACTT 420 CTCAGCTGTG AAAAATGTGA TTAAGTTGAG CCTCGAGATC TCCCTTTTCC TCAATAAACT 480 CCTGGTGCTG GGTGTGTCGG AATCCTCAAT CCACATCATT GGTGTTAGCC TGGGGGCCCA 540 CGTTGGGGGC ATGGTGGGAC AGCTCTTCGG AGGCCAGCTG GGACAGATCA CAGGCCTGGA 600 20 CCCCGCTGGA CCTGAGTACA CCAGGGCCAG TGTGGAAGAG CGCTTGGATG CTGGAGATGC 660 CCTCTTCGTG GAAGCCATCC ACACAGACAC CGACAATTTG GGTATTCGGA TTCCCGTTGG 720 ACATGTGGAC TACTTCGTCA ACGGAGGCCA AGACCAACCT GGCTGCCCCA CCTTCTTTTA 780 CGCAGGTTAT AGTTATCTGA TCTGTGATCA CATGAGGGCT GTGCACCTCT ACATCAGCGC 840 CCTGGAGAAT TCCTGTCCAC TGATGGCCTT TCCTGTGCC AGCTACAAGG CCTTCCTTGC 900 TGGACGCTGT CTGGATTGCT TTAACCCTTT TCTGCTTTCC TGCCCAAGGA TAGGACTGGT 960 GGAACAAGGT GGTGTCAAGA TAGAGCCGCT CCCCAAGGAA GTGAAAGTCT ACCTCCTGAC 1020 ū TACTTCCAGT GCTCCGTACT GCATGCATCA CAGCCTCGTG GAGTTTCACT TGAAGGAACT 1080 GAGAAACAAG GACACCAACA TCGAGGTTAC CTTCCTTAGC AGTAACATCA CCTCTTCATC 1140 TAAGATCACC ATACCTAAGC AGCAACGCTA TGGGAAAGGA ATCATAGCCC ATGCCACCCC 1200 ACAATGCCAG ATAAACCAAG TGAAATTCAA GTTTCAGTCT TCCAACCGAG TTTGGAAAAA 1260 AGACCGGACT ACCATTATTG GGAAGTTCTG CACTGCCCTT TTGCCTGTCA ATGACAGAGA 1320 1 þ AAAGATGGTC TGCTTACCTG AACCAGTGAA CTTACAAGCA AGTGTGACTG TTTCCTGTGA 1380 CCTGAAGATA GCCTGTGTGT AGTTTAACCT GGGCAGGACA CATCTCCCTG CATTTTTTT 1440 **35** TACTACTAAG GAGAAAAGCA AAGCTCTTTC TTATTTTCCT CATAATCAGC TACCCTGGAG 1560 GGGAGGGAGA ACTCATTTTA CAGAACTTGG TTTCCTTTGC CGATCTTATG TACATACCCA 1620 TTTTAGCTTT CCCATGCATA CTTAACTGCA CTTGCTTTAT CTCCTTGGGC ATTCGTACTT 1680 AGGATTCAAT AGAAACATGT ACAGGGTAAA CAATTTTTTA AAAATAAAAC TTCATGGAGT 1740 j. ΑΑΑΑΑΑΑΑΑ ΑΑΑΑΑΑΑ **40** 1 SEQ ID NO:128 PFH8 Protein sequence: NP_056984.1 TU Protein Accession #: 45 11 31 41 51 14 MPPGPWESCF WVGGLILWLS VGSSGDAPPT PQPKCADFQS ANLFEGTDLK VQFLLFVPSN 60 PSCGQLVEGS SDLQNSGFNA TLGTKLIIHG FRVLGTKPSW IDTFIRTLLR ATNANVIAVD 120 WIYGSTGVYF SAVKNVIKLS LEISLFLNKL LVLGVSESSI HIIGVSLGAH VGGMVGQLFG 180 50 GQLGQITGLD PAGPEYTRAS VEERLDAGDA LFVEAIHTDT DNLGIRIPVG HVDYFVNGGQ 240 DQPGCPTFFY AGYSYLICDH MRAVHLYISA LENSCPLMAF PCASYKAFLA GRCLDCFNPF 300 LLSCPRIGLV EQGGVKIEPL PKEVKVYLLT TSSAPYCMHH SLVEFHLKEL RNKDTNIEVT 360 FLSSNITSSS KITIPKQQRY GKGIIAHATP QCQINQVKFK FQSSNRVWKK DRTTIIGKFC 420 TALLPVNDRE KMVCLPEPVN LQASVTVSCD LKIACV 55 SEQ ID NO:129 PFH7 DNA SEQUENCE Nucleic Acid Accession #: NM_014384 60 89-1336 (underlined sequences correspond to start and stop codons) Coding sequence: 21 31 41 65 CGTTGCCGGG TCGCAGGTCC CGCCAGTGCG AGCGCAACGG AGGTCGAAGG CGTTCAGACT 60 CTTAGCTGAA CGCGGAGCTG CGGCGGCT \underline{AT} \underline{G} CTGTGGAGC GGCTGCCGGC GTTTCGGGGC 120 GCGCCTCGGC TGCCTGCCCG GCGGTCTCCG GGTCCTCGTC CAGACCGGCC ACCGGAGCTT 180 GACCTCCTGC ATCGACCCTT CCATGGGACT TAATGAAGAG CAGAAAGAAT TTCAAAAAGT 240 GGCCTTTGAC TTTGCTGCCC GAGAGATGGC TCCAAATATG GCAGAGTGGG ACCAGAAGGA 300 70 GCTGTTCCCA GTGGATGTGA TGCGGAAGGC AGCCCAGCTA GGCTTCGGAG GGGTCTACAT 360 ACAAACAGAT GTGGGCGGGT CTGGGCTGTC ACGTCTTGAT ACCTCTGTCA TTTTTGAAGC 420 CTTGGCTACA GGCTGCACCA GCACCACAGC CTATATAAGC ATCCACAACA TGTGTGCCTG 480 GATGATTGAT AGCTTCGGAA ATGAGGAACA GAGGCACAAA TTTTGCCCAC CGCTCTGTAC 540 CATGGAGAAG TTTGCTTCCT ACTGCCTCAC TGAACCAGGA AGTGGGAGTG ATGCTGCCTC 600 75 TCTTCTGACC TCCGCTAAGA AACAGGGAGA TCATTACATC CTCAATGGCT CCAAGGCCTT 660 CATCAGTGGT GCTGGTGAGT CAGACATCTA TGTGGTCATG TGCCGAACAG GAGGACCAGG 720 CCCCAAGGGC ATCTCATGCA TAGTTGTTGA GAAGGGGACC CCTGGCCTCA GCTTTGGCAA 780 GAAGGAGAAA AAGGTGGGGT GGAACTCCCA GCCAACACGA GCTGTGATCT TCGAAGACTG 840

TGCTGTCCCT GTGGCCAACA GAATTGGGAG CGAGGGGCAG GGCTTCCTCA TTGCCGTGAG 900

SEQ ID NO:127 PFH8 DNA SEQUENCE

AGGACTGAAC GGAGGGAGGA TCAATATTGC TTCCTGCTCC CTGGGGGCTG CCCACGCCTC 960 TGTCATCCTC ACCCGAGACC ACCTCAATGT CCGGAAGCAG TTTGGAGAGC CTCTGGCCAG 1020 TAACCAGTAC TTGCAATTCA CACTGGCTGA TATGGCAACA AGGCTGGTGG CCGCGCGGCT 1080 GATGGTCCGC AATGCAGCAG TGGCTCTGCA GGAGGAGGAGG AAGGATGCAG TGGCCTTGTG 1140 5 CTCCATGGCC AAGCTCTTTG CTACAGATGA ATGCTTTGCC ATCTGCAACC AGGCCTTGCA 1200 GATGCACGGG GGCTACGGCT ACCTGAAGGA TTACGCTGTT CAGCAGTACG TGCGGGACTC 1260 CAGGGTCCAC CAGATTCTAG AAGGTAGCAA TGAAGTGATG AGGATACTGA TCTCTAGAAG 1320 CCTGCTTCAG GAG<u>TAG</u>AACC CACACTTGTT CTGGCCTGGT GTTCAGTGCG ACTGCAGTCA 1380 GTGTTGAGTG GTGCCATGTG GGCCGCTCTA TTCCAAAGGA ATCATGGATT AGACCCAAGG 1440 GCTGAGCTCC TCTAGGGCAG GACCTGCACC CTGTGTGTTG GCACCAGCAT CGGGTCTTGG 1500 10 ACTGGGGCAG AATCCCCAGT GGAACCGGAA GAGCTGGACT GATGAGAAAC ATCAGAAGAA 1560 CACATACTAC CTTGTTTTCC TAATGCCAGA AGGGTGACCA GTGAAGATTC ACCGTCAAAC 1620 CATGAAAGTC CTTTCTTGGA TCCACTTTAT CTTGATTAGT CTGCATTTTA CTAGTTCACT 1680 GGATCCCTCC TCTAGGGGCC TGGGGACTTT CACTGATGCT CTTCCTGATT CTAGAGCAAA 1740 15 GGTGTGGGAA GGGGAAATGG AGGAATGCCC TCCTGTCTGT GTCGTTCTCT GTGCCACAGC 1800 TACAGATGCA GAAGGTTTCT CTGGATAGCA CACCTCTGAA TGTAAATCAT GATAAAATGG 1860 ATATTTGGAA ACTTACTCCT AAGCTGTGAT GTAGGGTGTA TTTCTACTTC TGGACTGCCT 1920 CAATATCAAG GGCTGAGACT TTTGAATGTT GAATATTCGT TGGGTTTCAT GTTAAGACGC 1980 CTGTGGTCCA GGAGTGCTAT TCAGTGTTTC TGTTCCTGAT AAACACTTTG AATATTTTTT 2040 20 TGTGTTTTTG TTTCCTTTTC TGAAGCTGTT CCTCCTTTTA AATATTTTTA ATCACATTGA 2100 TAAAATCTAT CCTTCATCCA CCTCTGGTTC TACTATAGTT GATTTTTATT TTAAATGTTT 2160 AATTGTATTT GATTAAACAC TTAACTGGAT TITTGGAATAA TAAAACTCTC GTCCAATTTG 2220 GCTTTTAAAA AAAAAAAA

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MLWSGCRRFG ARLGCLPGGL RVLVQTGHRS LTSCIDPSMG LNEEQKEFQK VAFDFAAREM 60
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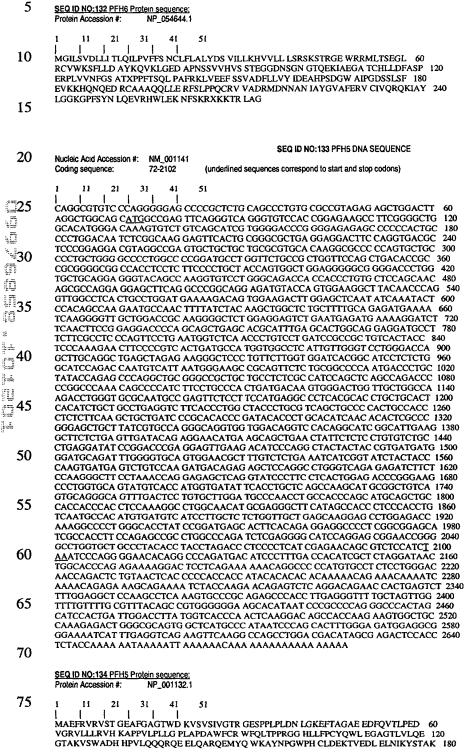
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Coding sequence: NM_013989
707-1105(underlined sequences correspond to start and stop codons)

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CATAGAGACA ATGAAAGGCT AAAGAAAATT TTAAAATCTC TGCCACAGTC TCATAGGTGC 300 TTGGAAATGA AAGTAGAACT GCCTGTCTTT AACGGACTCT GACAGAGGTA ACTGGATTAG 360 AAAAAAAAA AAAAAAAAA AAAAGGCAGC AGCTCCGAAT TGAATGAATT GATGGGCACA CTCCAACTGC TGGGCTGGAG AGACTGGACT TAGTCTTGCC ATTTCTGCTT CTTTGAAAGA 540 GGAGACAACT TGGGCTTCCT TTTAATTTAG TTTTTTTTCC CCTTCTCCCC CAACCCCCAA 600 CCTTCCCCCT TACCTCCCCC ACCCCCTTTA TCACCACCCC CCTTTTAAAT AAGAGGGTGA 660 AGGGGAACCA GAGCGCACAA GGGAACTGAC TCAGGAGGCA GAGAAG<u>ATG</u>G GCATCCTCAG CGTAGACTTG CTGATCACAC TGCAAATTCT GCCAGTTTTT TTCTCCAACT GCCTCTTCCT 780 GGCTCTCTAT GACTCGGTCA TTCTGCTCAA GCACGTGGTG CTGCTGTTGA GCCGCTCCAA 840 GTCCACTCGC GGAGAGTGGC GGCGCATGCT GACCTCAGAG GGACTGCGCT GCGTCTGGAA 900 GAGCTTCCTC CTCGATGCCT ACAAACAGGT GAAATTGGGT GAGGATGCCC CCAATTCCAG 960 TGTGGTGCAT GTCTCCAGTA CAGAAGGAGG TGACAACAGT GGCAATGGTA CCCAGGAGAA 1020 GATAGCTGAG GGAGCCACAT GCCACCTTCT TGACTTTGCC AGCCCTGAGC GCCCACTAGT 1080 GGTCAACTTT GGCTCAGCCA CTTGACCTCC TTTCACGAGC CAGCTGCCAG CCTTCCGCAA 1140 ACTGGTGGAA GAGTTCTCCT CAGTGGCTGA CTTCCTGCTG GTCTACATTG ATGAGGCTCA 1200 TCCATCAGAT GGCTGGGCGA TACCGGGGGA CTCCTCTTTG TCTTTTGAGG TGAAGAAGCA 1260 CCAGAACCAG GAAGATCGAT GTGCAGCAGC CCAGCAGCTT CTGGAGCGTT TCTCCTTGCC 1320 GCCCCAGTGC CGAGTTGTGG CTGACCGCAT GGACAATAAC GCCAACATAG CTTACGGGGT 1380 AGCCTTTGAA CGTGTGTGCA TTGTGCAGAG ACAGAAAATT GCTTATCTGG GAGGAAAGGG 1440 CCCCTTCTCC TACAACCTTC AAGAAGTCCG GCATTGGCTG GAGAAGAATT TCAGCAAGAG 1500 ATGAAAGAAA ACTAGATTAG CTGGTTAAAG GTATGATTAT AAGAGAGCTT ATTGTTTTAA 1560 AAAGTTATAT AAAGGCAAGG AAATTAAGAA CTGAATCCAT ATTTCAACAG AGCCCTATTG 1620 GCTTACTGAA AGACAGGAGT TTATCTATCG GAAGAACATG AATCTCTAAC AGCTCCATAC 1680 TTCTTTCACT ACTCAAATGG CATTGGGCTG AGTAAGTAAC CATATCACCT CTCTTCTTAG 1740 TAAAAAGCCC TATGTGAAAA GATCCCAAGA TGGAGAGGAA GAAACGCTAA TTCAGCATGT 1800 GTTCATTCTG CATTGAGAAG GAACTGATAC ATCTGATGCA TGCTTTGAGA CCAGAAGAAA 1860 AGACTTACCT GAATAATTAC TACATTAGGG AAGCTACTGT CTACGTTAAG ATAAAGGGTA 1920

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GATTATAGCT CCCAAAAGAA TGGACCAACC ACTTTCGTAT CATAATTTCT TTTTGGTAAA 3180 TATGAGACTA TTATGAAATC ATAGTATATG ATTGTATTTA AAGGTACAAT CAAAGGATCT 3240 TTTGTCCATT CCATTAATAA CTGAATAAAA AATAAATAAA ATGGATAGAA AAAAACTAAA 3300 GTTGAAAATA CATTCTTAAA CTAGTTGTCT GAAATGAGAA AAGAGTGAGA ACTAGGTGTG 3360 25 CAAGAACCAA ACGTATITTA TTTTATTTTT TAAATGGGAG CAACATATCA GTCGTGTCAC 3420 CAGCTGGTAT ATTGTGTAAA TATTAAAGCT CCATTGGGAC TGATTTTTCA TGGCAACATC 3480 AGCTTTCTAA TGTTCTAAAT TCTATAAAAA CCACCCACAA AGAAACAAAG CAAATTTCAT 3540 1 į TATCTAATGA GTTGCTGGAA AATCATATTG AGAATAATTA TTTCAGATTC CTCAGTTGTT 3600
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TTCTCTCATC ACAGTGGGAA GAATAGCCTA TTGTCTTTCA TTTTGCCTGA GTGTATTTTA 4980 50 CTATTTGGGC TCTGAAATAA AAATTATGAA ATATGGTGAG GTCACATGTT GGTGCTGCCT 5040 TGCTGCATAA AATTCTAGGA GGGCAGGTTA GGAGACAGTT ATGTATGGCC TTTCGGGAAA 5100 ATTCAAAGGG TGGGATTACA AGGGTGTTCC TCAGGCATGC CCCTATGGGC CCTATGTGGA 5160 55 AGCAAGAAGA ATTGACTGAT TTACAGGACT TCTCTTTATG TCAATCTTAA GAGGATGGAT 5220 GAATCTGGAC ATTTGTTCCA CCCGACCTCT GACTGATGGT TTGGAAAATA ACTTTAATTA 5280 GGATCATATG ACCATTGAAA AAGGAAAAAT GTAGACTCTG ACTTCCGTCC CACTGAAGGA 5340 TTAATGAAAA CCTTTACTAG CATTTAGAGC TTTTCAGAAC ATCCCCACTG TCATGTGTCT 5400 CAGCAGTGGA GACTGCAAGT AAGGCTTTTA ATTTTAGGAG GTTTTTTTTT TTTTTTTTT 5460 60 TTCCCCTAAA TGGTATGGCC AAAAGTCAGA GTTAAAATAT ATATAGTTAG ATTCCAACTT 5520 CCTCCTTCAC TCTAAAAATA GAATCCAAAC CCACTCTTCA TATATGCTTC CAGAATGGGG 5580 CTTAAGTACC AATCTCTGCT TTGCAATGGG CACAATCTTG GTCATGTCCT GAGGCTCTCT 5640 AAGAAAAGAG AGGATCTAGG ATGGGAGAGC TAGAAAGTTG CTAACTGGGA AGAACAAGGC 5700 CCTGAGGGGT TGGTCTACCA ATCTGGGAAG ATTTGAAAAC AAACTTCTCG CAACTGAAGG 5760 65 AAGGCTGAAG GCTGCTGCAA GTCATTGAGT GACTTTAGGA TGAGCAAAAC ATTGGGCCAC 5820 TTCCTAATGC CCTATGTGTA TAGTACCAGA AGCAAGGTCT CAGACTTAAC AGACCCAGCT 5880 CTGTTCCAAG GTGAGTCTGA ACCAATAGAA AGCAAACATG TGCAGATATC CAAACAAGAC 5940 TGCTCATGCA AGTCGGGGCT GGCTACCCGT CTTAGGCAGC AACAGCAGAG CTCCAGGGAG 6000 CTTATTCAAT ATTTACTGAG ACTTCGAAGA CCCAGCAGAT GTTTAATGAA GTCACTATTT 6060 70 TGGCTCAAAC CCTCCACTTC TCCCCCTCCC CTCAAAAAGC CAACAGGTAA ACACATAAAT 6120 GAAAGAAACC CACAGAAGGG GATGGGAAAT AAAGAAAATT CTCTCAAGAC TTCTCCAGGC 6180 CCATGTCACT GGTCAGCGTG GTTTTTATGT GTATTAGGAT TGGGGGATGT GAAGAAATAA 6240 GTATCCAGTA CTTTATAACC AAAGCAATTA AATGATATTG GGGTAGGGAA TGTTGGCCAG 6300 TTTTGTTTAG TTTTGCCATC ACATTGTCAC CCAGACCTCA CCTAGCCCCA AGTAATCGGG 6360 75 CGCCCCGAAG AGGGAGACAG AGATGTGCCA GAGTTGACCC AGTGTGCGGA TGATAACTAC 6420 TGACGAAAGA GTCATCGACC TCAGTTAGTG GTTGGATGTA GTCACATTAG TTTGCCTCTC 6480 CCCATCTTTG TCTCCCTGGC AAGGAGAATA TGCGGGACAT GATGCTAAGA GCCCTGGGTA 6540 AATGTGGTGA GAATGCACGC GTGCATATGC TACACATATG TGCTTCTCAG TTGCAGAAAA 6600 TGAACTGCTT TGGGAGATTA TCAGTAGAAA GAGTGTTATC ATATTGGTGC TGAGTGCTAT 6660

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SEQ ID NO:135 PFH4 DNA SEQUENCE

Nucleic Acid Accession #: NM_002742
Coding sequence: 236-2974 (underlined sequences correspond to start and stop codons)

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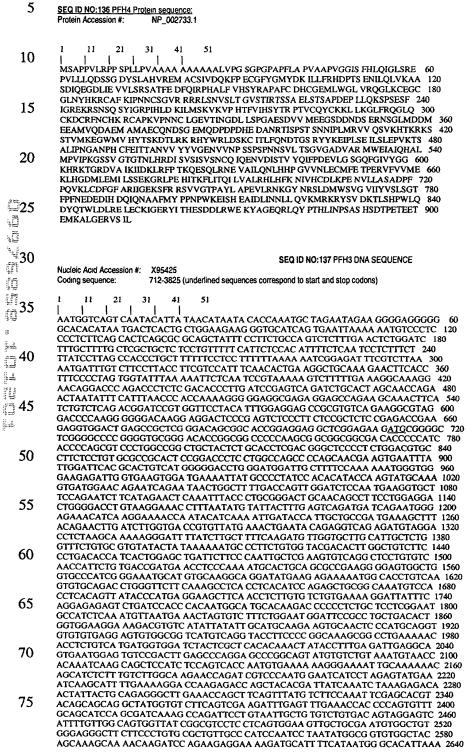
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TATGGAAAAT CAGCTGCTCA GCAACCTTTC ACCTTTGTGT ATTTTTCAAT AATAAAAAA 3720 ATTCTTGTCA AAAAAAAAA AA



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Nucleic Acid Accession #: NM_016029

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21 31 41 51 MRGSGPRGAG HRRPPSGGGD TPITPASLAG CYSAPRRAPL WTCLLLCAAL RTLLASPSNE 60 VNLLDSRTVM GDLGWIAFPK NGWEEIGEVD ENYAPIHTYQ VCKVMEQNQN NWLLTSWISN 120 EGASRIFIEL KFTLRDCNSL PGGLGTCKET FNMYYFESDD QNGRNIKENQ YIKIDTIAAD 180 ESFTELDIGD RVMKLNTEVR DVOPLSKKGF YLAFQDVGAC IALVSVRVYY KKCPSVVRHL 240 AVFPDTITGA DSSQLLEVSG SCVNHSVTDE PPKMHCSAEG EWLVPIGKCM CKAGYEEKNG 300 TCQVCRPGFF KASPHIQSCG KCPPHSYTHE EASTSCVCEK DYFRRESDPP TMACTRPPSA 360 PRNAISNVNE TSVFLEWIPP ADTGGRKDVS YYIACKKCNS HAGVCEECGG HVRYLPRQSG 420 LKNTSVMMVD LLAHTNYTFE IEAVNGVSDL SPGARQYVSV NVTTNQAAPS PVTNVKKGKI 480 AKNSISLSWQ EPDRPNGIIL EYEIKHFEKD QETSYTIIKS KETTITAEGL KPASVYVFQI 540 RARTAAGYGV FSRRFEFETT PVFAASSDQS QIPVIAVSVT VGVILLAVVI GVLLSGSCCE 600 CGCGRASSLC AVAHPILIWR CGYSKAKQDP EEEKMHFHNG HIKLPGVRTY IDPHTYEDPN 660 QAVHEFAKEI EASCITIERV IGAGEFGEVC SGRLKLPGKR ELPVAIKTLK VGYTEKQRRD 720 FLGEASIMGQ FDHPNIIHLE GVVTKSKPVM IVTEYMENGS LDTFLKKNDG QFTVIQLVGM 780 LRGISAGMKY LSDMGYVHRD LAARNILINS NLVCKVSDFG LSRVLEDDPE AAYTTRGGKI 840 PIRWTAPEAI AFRKFTSASD VWSYGIVMWE VVSYGERPYW EMTNQDVIKA VEEGYRLPSP 900 MDCPAALYQL MLDCWQKERN SRPKFDEIVN MLDKLIRNPS SLKTLVNASC RVSNLLAEHS 960 PLGSGAYRSV GEWLEAIKMG RYTEIFMENG YSSMDAVAOV TLEDLRRLGV TLVGHOKKIM 1020 NSLQEMKVQL VNGMVPL

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TATGGGCCGA GTGGCAGGGA CGACGCCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240 TGACTGGAGC CTCGAGTGGA ATTGGTGAGG AGCTGGCTTA CCAGTTGTCT AAACTAGGAG 300 65 TTTCTCTTGT GCTGTCAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360 TAGAGAATGG CAATTTAAAA GAAAAAGATA TACTTGTTTT GCCCCTTGAC CTGACCGACA 420 CTGGTTCCCA TGAAGCGGCT ACCAAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
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ACTITITAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260 AGATTGCCAT GAATCTTGCA AA 5 SEQ ID NO:140 PFH2 Protein sequence: Protein Accession #: 41 51 10 GIGEELAYQL SKLGVSLVLS ARRVHELERV KRRCLENGNL KEKDILVLPL DLTDTGSHEA 120 ATKAVLQEFG RIDILVNNGG MSQRSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHMIER 180 KQGKIVTVNS ILGIISVPLS IGYCASKHAL RGFFNGLRTE LATYPGIIVS NICPGPVQSN 240 15 IVENSLAGEV TKTIGNNGDQ SHKMTTSRCV RLMLISMAND LKEVWISEQP FLLVTYLWQY 300 MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD 20 SEQ ID NO:141 PFH1 DNA SEQUENCE Nucleic Acid Accession #: NM 021614 1-1740 (underlined sequences correspond to start and stop codons) Coding sequence: 21 31 **25** ATGAGCAGCT GCAGGTACAA CGGGGGCGTC ATGCGGCCGC TCAGCAACTT GAGCGCGTCC 60 L CGCCGGAACC TGCACGAGAT GGACTCAGAG GCGCAGCCCC TGCAGCCCCC CGCGTCTGTC 120 __ GGAGGAGGTG GCGCCGCTC CTCCCCGTCT GCAGCCGCTG CCGCCGCCGC CGCTGTTTCG 180 TCCTCAGCCC CCGAGATCGT GGTGTCTAAG CCCGAGCACA ACAACTCCAA CAACCTGGCG 240 CTCTATGGAA CCGGCGGCGG AGGCAGCACT GGAGGAGGCG GCGGCGGTGG CGGGAGCGGG 300 7 CACGGCAGCA GCAGTGGCAC CAAGTCCAGC AAAAAGAAAA ACCAGAACAT CGGCTACAAG 360 CTGGGCCACC GGCGCGCCCT GTTCGAAAAG CGCAAGCGGC TCAGCGACTA CGCGCTCATC 420 TTCGGCATGT TCGGCATCGT GGTCATGGTC ATCGAGACCG AGCTGTCGTG GGGCGCCTAC 480 35 GACAAGGCGT CGCTGTATTC CTTAGCTCTG AAATGCCTTA TCAGTCTCTC CACGATCATC 540 CTGCTCGGTC TGATCATCGT GTACCACGCC AGGGAAATAC AGTTGTTCAT GGTGGACAAT 600 GGAGCAGATG ACTGGAGAAT AGCCATGACT TATGAGCGTA TTTTCTTCAT CTGCTTGGAA 660 ATACTGGTGT GTGCTATTCA TCCCATACCT GGGAATTATA CATTCACATG GACGGCCCGG 720 CTTGCCTTCT CCTATGCCCC ATCCACAACC ACCGCTGATG TGGATATTAT TTTATCTATA 780 CCAATGTTCT TAAGACTCTA TCTGATTGCC AGAGTCATGC TTTTACATAG CAAACTTTTC 840 ACTGATGCCT CCTCTAGAAG CATTGGAGCA CTTAATAAGA TAAACTTCAA TACACGTTTT 900 40 GTTATGAAGA CTTTAATGAC TATATGCCCA GGAACTGTAC TCTTGGTTTT TAGTATCTCA 960 14 TTATGGATAA TTGCCGCATG GACTGTCCGA GCTTGTGAAA GGTACCATGA TCAACAGGAT 1020 GTTACTAGCA ACTTCCTTGG AGCGATGTGG TTGATATCAA TAACTTTTCT CTCCATTGGT 1080 [] ___ 45 TATGGTGACA TGGTACCTAA CACATACTGT GGAAAAGGAG TCTGCTTACT TACTGGAATT 1140 ATGGGTGCTG GTTGCACAGC CCTGGTGGTA GCTGTAGTGG CAAGGAAGCT AGAACTTACC 1200 AAAGCAGAAA AACACGTGCA CAATTTCATG ATGGATACTC AGCTGACTAA AAGAGTAAAA 1260 AATGCAGCTG CCAATGTACT CAGGGAAACA TGGCTAATTT ACAAAAATAC AAAGCTAGTG 1320 AAAAAGATAG ATCATGCAAA AGTAAGAAAA CATCAACGAA AATTCCTGCA AGCTATTCAT 1380 CAATTAAGAA GTGTAAAAAT GGAGCAGAGG AAACTGAATG ACCAAGCAAA CACTTTGGTG 1440 50 GACTTGGCAA AGACCCAGAA CATCATGTAT GATATGATTT CTGACTTAAA CGAAAGGAGT 1500 GAAGACTTCG AGAAGAGGAT TGTTACCCTG GAAACAAAAC TAGAGACTTT GATTGGTAGC 1560 ATCCACGCCC TCCCTGGGCT CATAAGCCAG ACCATCAGGC AGCAGCAGAG AGATTTCATT 1620 GAGGCTCAGA TGGAGAGCTA CGACAAGCAC GTCACTTACA ATGCTGAGCG GTCCCGGTCC 1680 TCGTCCAGGA GGCGGCGGTC CTCTTCCACA GCACCACCAA CTTCATCAGA GAGTAGCTAG 55 SEQ ID NO:142 PFH1 Protein sequence: Protein Accession #: NP_067627 60 | | | | | | | MSSCRYNGGV MRPLSNLSAS RRNLHEMDSE AQPLQPPASV GGGGGASSPS AAAAAAAAA 60 SSAPEIVVSK PEHNNSNNLA LYGTGGGGST GGGGGGGGGG HGSSSGTKSS KKKNQNIGYK 120 LGHRRALFEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180 65 LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIP GNYTFTWTAR 240 LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSKLF TDASSRSIGA LNKINFNTRF 300 VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQQD VTSNFLGAMW LISITFLSIG 360 YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFM MDTOLTKRVK 420 NAAANVLRET WLIYKNTKLV KKIDHAKVRK HQRKFLQAIH QLRSVKMEQR KLNDQANTLV 480 70

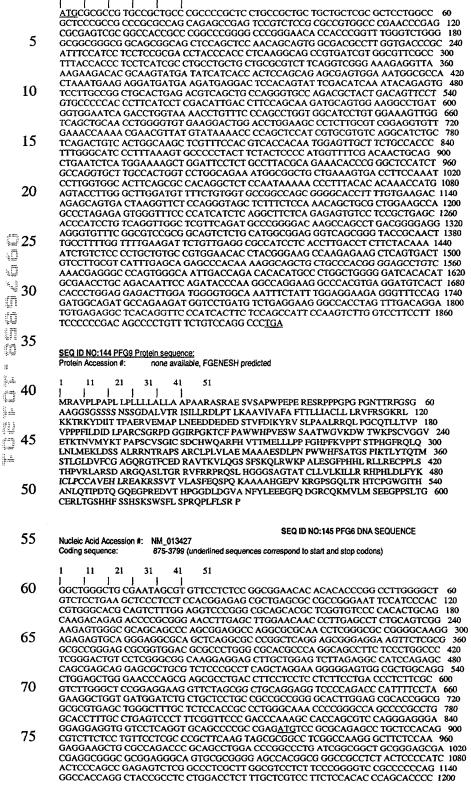
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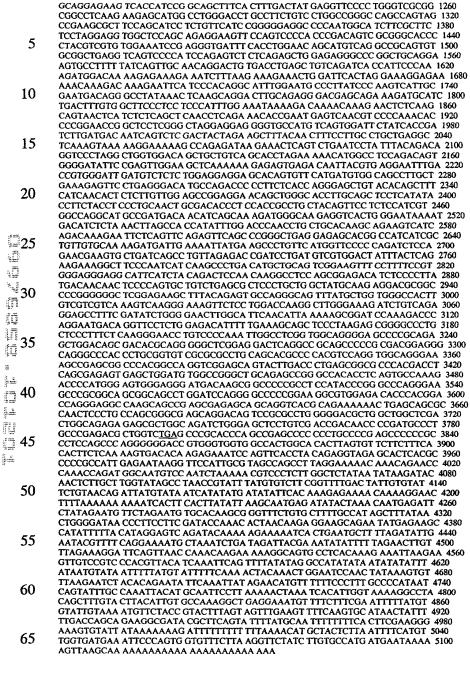
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DLAKTQNIMY DMISDLNERS EDFEKRIVTL ETKLETLIGS IHALPGLISQ TIRQQQRDFI 540

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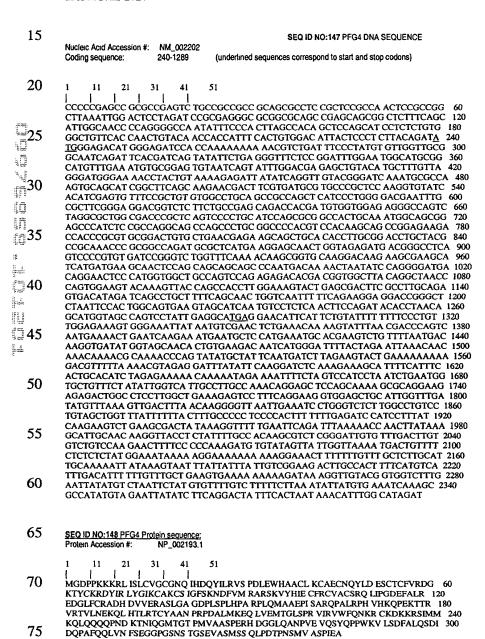


70 SEQ ID NO:146 PFG6 Protein sequence: Protein Accession #: NP_038286.1

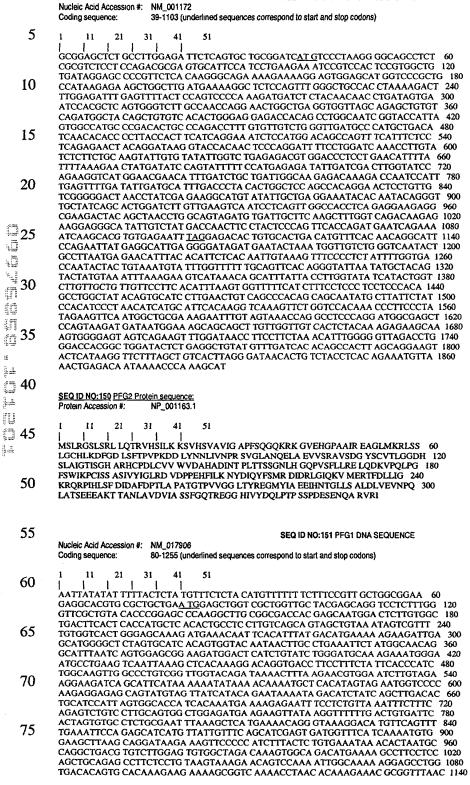
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⁷⁵ MSAQSLLHSV FSCSSPASSS AASAKGFSKR KLRQTRSLDP ALIGGCGSDE AGAEGSARGA 60
TAGRLYSPSL PAESLGPRLA SSSRGPPPRA TRLPPPGPLC SSFSTPSTPQ EKSPSGSFHF 120
DYEVPLGRGG LKKSMAWDLP SVLAGPASSR SASSILCSSG GGPNGIFASP RRWLQQRKFQ 180
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LSCQITPRD GQRRKKSLRK KLDSLGKEKN KDKEFIPQAF GMPLSQVIAN DRAYKLKQDL 300
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SEQ ID NO:149 PFG2 DNA SEQUENCE



SEQ ID NO:152 PFG1 Protein sequence: Protein Accession #: NP_060376.1

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MELVAGCYEQ VLFGFAVHPE PKACGDHEQW TLVADFTHHA HTASLSAVAV NSRFVVTGSK 60
DETHHYDMK KKIEHGALVH HSGTITCLKF YGNRHLISGA EDGLICIWDA KKWECLKSIK 120
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FKAHENRVKD MFSFEIPEHH VIVSASSDGF IKMWKLKQDK KVPPSLLCEI NTNARLTCLG 300
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SEQ ID NO:153 PFD6 DNA SEQUENCE

Nucleic Acid Accession #: NM_014668
Coding sequence: NIM_014668
110-2953 (underlined sequences correspond to start and stop codons)

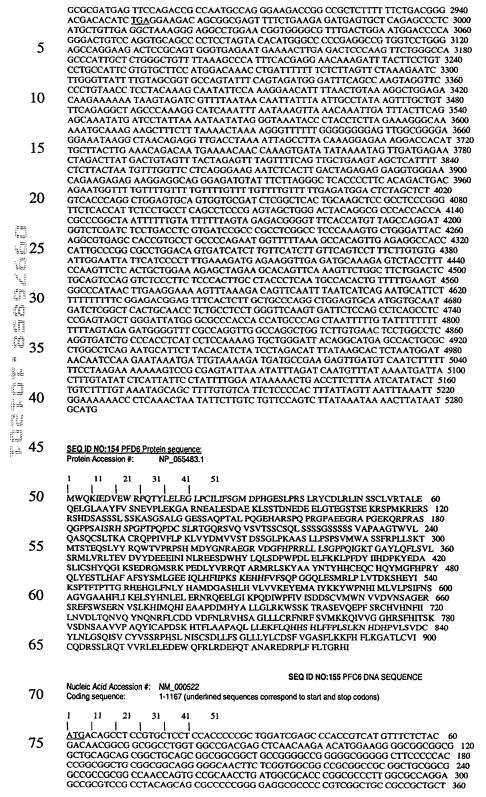
1 11 21 31 41 51

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CCTGATCTTC AGTGGGATGG ACCCGCATGG GGAGTCCTTG CCGAGGTCTT TGAGGTACTG 240 TGACCTGCGA TTGATAAACT CCTCCTGCTT GGTGAGAACA GCCTTGGAGC AGGAGCTGGG 300 CCTGGCTGCC TACTTTGTGA GCAACGAGGT TCCCTTGGAG AAGGGGGCTA GGAACGAGGC 360 CTTGGAGAGT GATGCTGAGA AGCTGAGCAG CACAGACAAC GAGGATGAGG AGCTGGGGAC 420
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CCCTCAGATC GGGAAGACAG GTGCCTACCT CCACCCCCCC AGGCTGCTGC TCAGCGGCCC 1140
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AGAATCTGAC TGGCATTATC TCCAGCTTAG CGACCCCTGG CCAGACCTGG AGCTGTTCAA 1320 GAAGTTGCCC TTTGACTACA TCATTCACGA CCCGAAGTAT GAAGATGCCA GCCTGATTTG 1380 TTCGCACTAT CAGGGTATAA AGAGTGAAGA CAGAGGGATG TCCCGGAAGC CGGAGGACCT 1440 TTATGTGCGG CGTCAGACGG CACGGATGAG ACTGTCCAAG TACGCAGCGT ACAACACTTA 1500 CTTCATCATC CCCAAGTCCA AGGAGCACCA CTTTGTCTTC AGCCAACCTG GAGGCCAGCT 1680 GGAGAGCATG CGACTACCCC TCGTGACAGA CAAGAGCCAT GAATATATAA AAAGTCCGAC 1740

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GCCGCGGCTG CCGCTGCAGC CGCCGCCGCC GCCGCCGCGT CGTCCTCGGG AGGTCCCGGC 420

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THAVQIALMA LKMMELSDEV MSPHGEPIKM RIGLHSGSVF AGVVGVKMPR YCLFGNNVTL 600 25 ANKFESCSVP RKINVSPTTY RLLKDCPGFV FTPRSREELP PNFPSEIPGI CHFLDAYQQG 660 TNSKPCFQKK DVEDASQFFR QSIRNRLATY IPIYKSLGFD SLKMCRASES TLGIVDG 30 SEQ ID NO:159 PFA1 DNA SEQUENCE Nucleic Acid Accession #: NM_004362 102-1934 (underlined sequences correspond to start and stop codons) Coding sequence: 35 51 CGCCGGCGG ACTGGTCTGA AGAGACGCGG GGACAAAGTG GCAACGACTT GGACATCTGA 60 GCTGTCACTG CCGAAAACAG GCCGCAAGAG AGATAATCAA TATGCATTTC CAAGCCTTTT 120 40 GGCTATGTTT GGGTCTTCTG TTCATCTCAA TTAATGCAGA ATTTATGGAT GATGATGTTG 180 AGACGGAAGA CTTTGAAGAA AATTCAGAAG AAATTGATGT TAATGAAAGT GAACTTTCCT 240 CAGAGATTAA ATATAAGACA CCTCAACCTA TAGGAGAAGT ATATTTTGCA GAAACTTTTG 300 ATAGTGGAAG GTTGGCTGGA TGGGTCTTAT CAAAAGCAAA GAAAGATGAC ATGGATGAGG 360 AAATTTCAAT ATACGATGGA AGATGGGAAA TTGAAGAGTT GAAAGAAAAC CAGGTACCTG 420 45 GTGACAGAGG ACTGGTATTA AAATCTAGAG CAAAGCATCA TGCAATATCT GCTGTATTAG 480 CAAAACCATT CATTTTTGCT GATAAACCCT TGATAGTTCA ATATGAAGTA AATTTTCAAG 540 ATGGTATTGA TTGTGGAGGT GCATACATTA AACTCCTAGC AGACACTGAT GATTTGATTC 600
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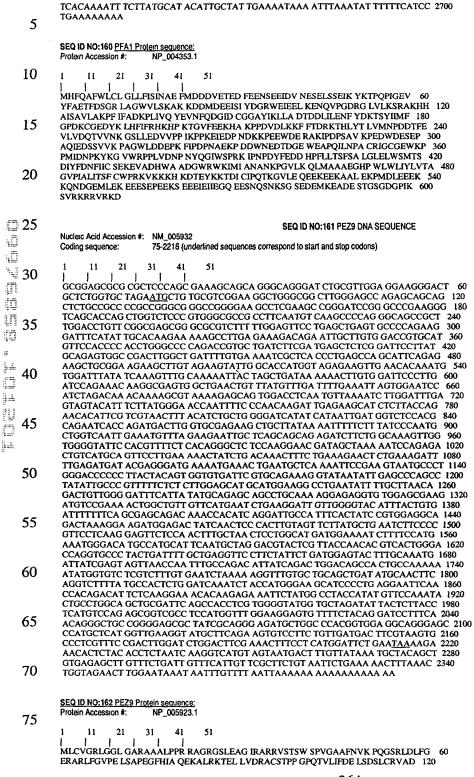
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SEQ ID NO:163 PEZ8 DNA SEQUENCE

Nucleic Acid Accession #: AF103907
Coding sequence: AF103907
none (underlined sequences correspond to start and stop codons)

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31 41 ACAGAAGAAA TAGCAAGTGC CGAGAAGCTG GCATCAGAAA AACAGAGGGG AGATTTGTGT 60 GGCTGCAGCC GAGGGAGACC AGGAAGATCT GCATGGTGGG AAGGACCTGA TGATACAGAG 120 GAATTACAAC ACATATACTT AGTGTTTCAA TGAACACCAA GATAAATAAG TGAAGAGCTA 180 GTCCGCTGTG AGTCTCCTCA GTGACACAGG GCTGGATCAC CATCGACGGC ACTTTCTGAG 240 TACTCAGTGC AGCAAAGAAA GACTACAGAC ATCTCAATGG CAGGGGTGAG AAATAAGAAA 300 GGCTGCTGAC TTTACCATCT GAGGCCACAC ATCTGCTGAA ATGGAGATAA TTAACATCAC 360 TAGAAACAGC AAGATGACAA TATAATGTCT AAGTAGTGAC ATGTTTTTGC ACATTTCCAG 420 CCCCTTTAAA TATCCACACA CACAGGAAGC ACAAAAGGAA GCACAGAGAT CCCTGGGAGA 480 AATGCCCGGC CGCCATCTTG GGTCATCGAT GAGCCTCGCC CTGTGCCTGG TCCCGCTTGT 540 GAGGGAAGGA CATTAGAAAA TGAATTGATG TGTTCCTTAA AGGATGGGCA GGAAAACAGA 600 TCCTGTTGTG GATATTTATT TGAACGGGAT TACAGATTTG AAATGAAGTC ACAAAGTGAG 660 CATTACCAAT GAGAGGAAAA CAGACGAGAA AATCTTGATG GCTTCACAAG ACATGCAACA 720 AACAAAATGG AATACTGTGA TGACATGAGG CAGCCAAGCT GGGGAGGAGA TAACCACGGG 780 GCAGAGGGTC AGGATTCTGG CCCTGCTGCC TAAACTGTGC GTTCATAACC AAATCATTTC 840 ATATTTCTAA CCCTCAAAAC AAAGCTGTTG TAATATCTGA TCTCTACGGT TCCTTCTGGG 900 CCCAACATTC TCCATATATC CAGCCACACT CATTTTTAAT ATTTAGTTCC CAGATCTGTA 960 CTGTGACCTT TCTACACTGT AGAATAACAT TACTCATTTT GTTCAAAGAC CCTTCGTGTT 1020 GCTGCCTAAT ATGTAGCTGA CTGTTTTTCC TAAGGAGTGT TCTGGCCCAG GGGATCTGTG 1080 AACAGGCTGG GAAGCATCTC AAGATCTTTC CAGGGTTATA CTTACTAGCA CACAGCATGA 1140 TCATTACGGA GTGAATTATC TAATCAACAT CATCCTCAGT GTCTTTGCCC ATACTGAAAT 1200 TCATTTCCCA CTTTTGTGCC CATTCTCAAG ACCTCAAAAT GTCATTCCAT TAATATCACA 1260 GGATTAACTT TTTTTTTAA CCTGGAAGAA TTCAATGTTA CATGCAGCTA TGGGAATTTA 1320 ATTACATATT TTGTTTTCCA GTGCAAAGAT GACTAAGTCC TTTATCCCTC CCCTTTGTTT 1380 GATTTTTTTT CCAGTATAAA GTTAAAATGC TTAGCCTTGT ACTGAGGCTG TATACAGCAC 1440 AGCCTCTCCC CATCCCTCCA GCCTTATCTG TCATCACCAT CAACCCCTCC CATACCACCT 1500 AAACAAAATC TAACTTGTAA TTCCTTGAAC ATGTCAGGAC ATACATTATT CCTTCTGCCT 1560
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10 PEZ8 Protein sequence:
Protein Accession #: none

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SEQ ID NO:164 PEZ6 DNA SEQUENCE

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GATGAAGGTG GGGTGGCGTG GCAAGCCGGA CTAAGGACCG GGGACTTCTT GATTGAGGTT 300
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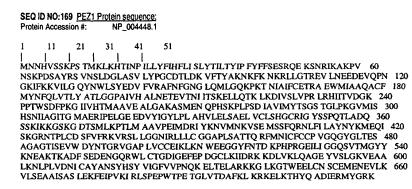
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	Nucleic Acid Acc		00.4075/	none found			
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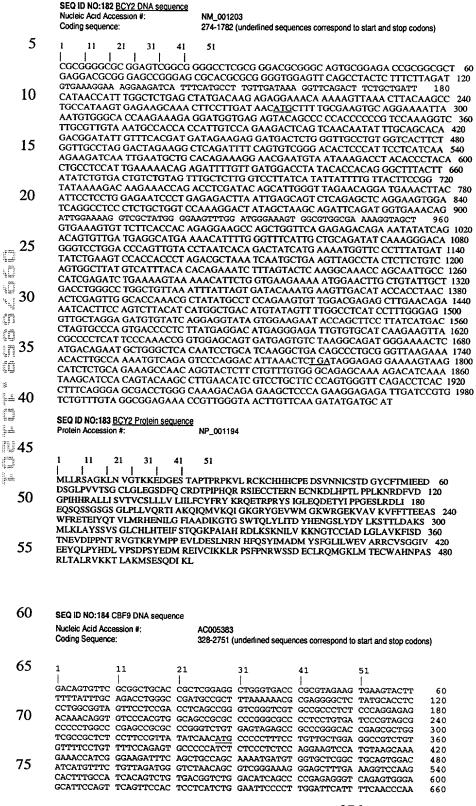
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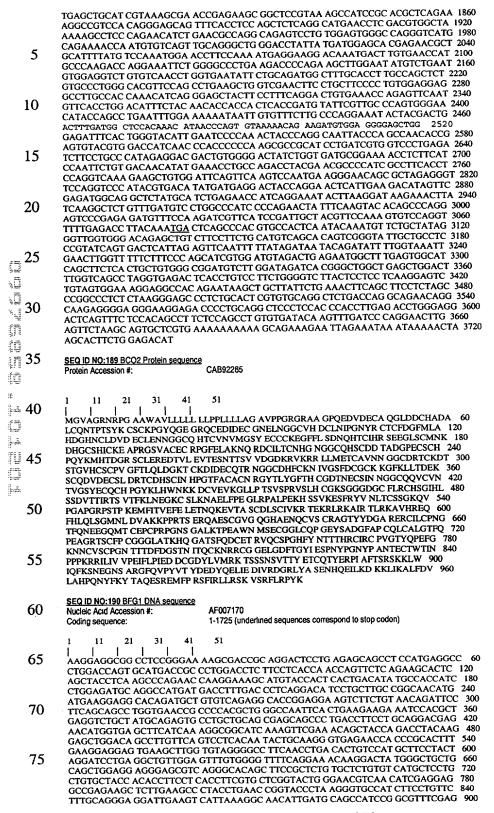
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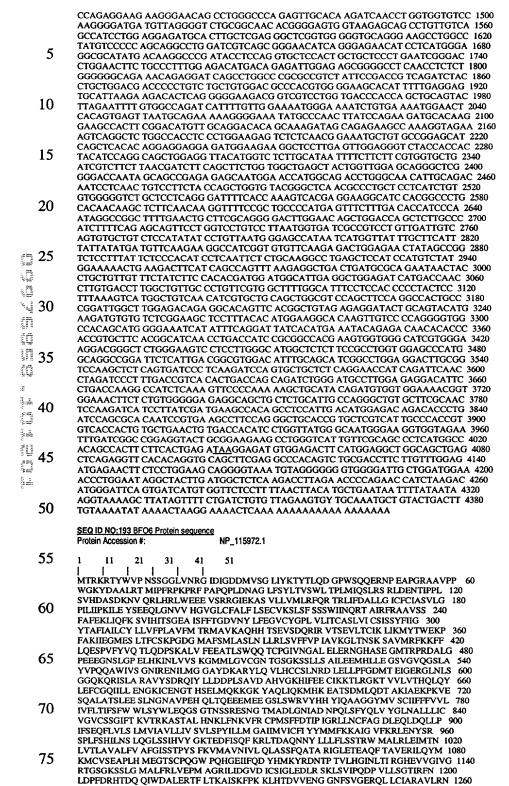
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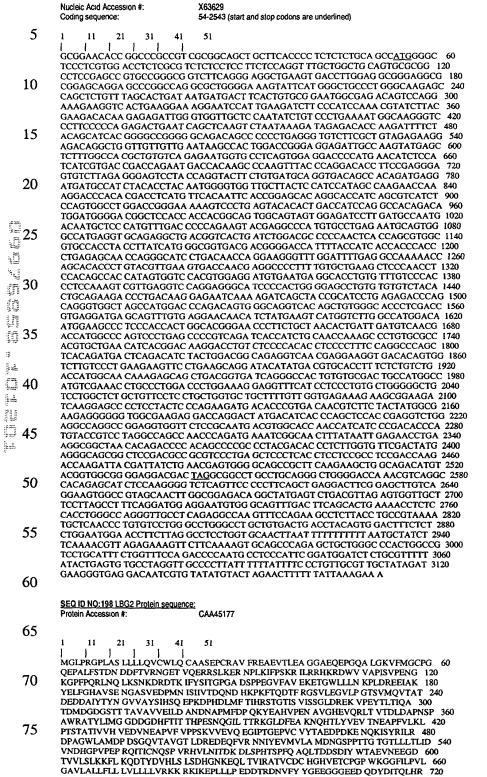
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The state of the s			TGGATTCGTC				1080
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íT	TAA						
-25 -10 -30 -11							
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14			FICIFFATCG				240
1145			NVFFGGNLSS				300
			LSEEPRTHSD E SHVQQTTQL		GAVVMVFGFV	MAITNTQDCT	360
Part.	HOQLMI ICI	DIVISERVISI	L SITT QQTTQL	3 ILINDII QLL			
10	Musicia Acad Acad	i #:	110000		0:213 PAV4 VAR	IANT 3 DNA SEQU	ENCE
50	Nucleic Acid Acce Coding sequence		N62096 1-1140		nces correspond to	o start and stop cod	ons)
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	1	11	21	31	41	51	
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55			GCCTGTCATC				60
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360

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	Coding sequence				ces correspond to	start and stop code	ns)
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				J CGIIRIIIC	<u> </u>		
	Protein Accession	<u>PBM2 Protein seq</u> n #:	uence: none fo	und			
35							
įū	1	11	21	31	41	51	
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					Q ID NO:229 PEZ	DNA SEQUENCE	:
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i i u	Nucleic Acid Acci Coding sequence	ession #: :: 11	NM_014253 65-8242 (under	SEC drined sequences of	correspond to start	and stop codons)	
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1 45	Nucleic Acid Acci Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATCTAGCT	ession #: 11 ATTAAAGGAC CAAACTGACT TACACCAGTT	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA	sed dined sequences of the sequence of the sequences of t	correspond to start 41 GAAACTGAGC CCAAAAGTCA GGAAGAAAAAC	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC	60 120 180
45	Nucleic Acid Acce Coding sequence 1	ession #: 11 ATTAAAGGAC CAAACTGACT	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAAC CTGAGGATGA	and stop codons) 51 i TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG	60 120
45	Nucleic Acid Accc Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATCTAGCT ATACAACTCC CCAGAGTAGA CTCTCACACT	ession #: 11 ATTANAGGAC CANACTGACT TACACCAGTT AGGGAGACCC AAGAGGANAG CTGTGCTCTG	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA GCTACCAAAC	31 TTTTTTCAT CCAGCCTCTA GAGTGAAGAT TAACCAGGAG ATCTACTCAA AGACATGCAC	41 { GAAACTGAGC CCAAAAGTCA GGAAGAAAC GGAAGAAAAAAAAAA	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA	60 120 180 240 300 360
45	Nucleic Acid According sequence 1	ession #: 11 ATTANAGGAC CANACTGACT TACACCAGT TACGGAGACCC ANGAGGANAG	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA AGCTACCAAAC ATGTGGACAC	31 TTTTTTCAT CAGCCTCTA GAGTGAAGAT TAACCAGGAG ATCTACTCAA AGACATGCAC AGAGACAGAA	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAAC CTGAGGATGAA AGCGTTTCTC GGTGCTGCCT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAG TCTGTGAAAG CACCTGACCA	60 120 180 240 300
45	Nucleic Acid Acci Coding sequence 1	ession #: 11 ATTANAGGAC CAACTGACT TACACCAGTT AGGAGACCC AAGAGGAAAG CTGTGCTCTG ATGTGGATCTG ATGTGGATCAAGGGATTAAGGGATTAAGGGATTAAGGGATTAAGGGATTATCCT	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TTCCACGAGTA AAGTAGAAAA GCTACCAAAC ATGTGGACAA TGGGGGAATGAA TGACTGACAC	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAAC CTGAGGATGA GAGATGGAAT AGCGTTTCTC GGTGCTGCCT AGGAAGTCTTC	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA ATGCCCG ATGGGGAAAA	60 120 180 240 300 360 420 480 540
50 55	Nucleic Acid Acce Coding sequence 1	ession #: 11 ATTANAGGAC CANACTGACT TACACCAGTT AGGGAGACC AGAGGANAG CTGTGCTCTG ATGGGATCTG ATGTGGATCA ACCACTATACCT ATGTGGATCAC ACCACACACA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAC ATGTGGACAC GGGGAATGAA TGACTGACAC GGGGAATGAA ACCAGTTCAC	dined sequences of the sequence of the seq	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAAC CTGAGGATGA AGGATGCAAT AGGATGTTCTC GGTGCTGCT AGTACTGTT AGGAAGTCTGT AGGAAGTCGT CAAGCTGGGT CTCCCACCGC	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA TGTCCAGCCG ATGGGGAAAA CTACTCAAGA CACCTCCACCC	60 120 240 300 360 420 480 540 600 660
45	Nucleic Acid According sequence 1	ession #: 11 ATTANAGGAC CAACTGACT TACACCAGTT AGGGAGACCC AAGAGGANAG CTGTGCTCTG ATTGGATCTG ATTGGATAA GCATTATCCT TTCTCTCTCTG TGCACCACA TGCACCTGTG	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA ACTTCTGATGA TCCACGAGTA AAGTAGAAAA GCTACCAAAC GGGGAATGAA TGACTGACAC TTTGTTGTGA ACCAGTTCAC CCAGGAAGCC CCAGGAAGCC	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAA CTGAGGATGA GGATGAAT AGGGTTTCTC GGTGCTGCCT AGGAAGTCTG CAAGCTGGGT CTCCCACCGC GCGGACTCTC	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGACTA CACCTGACCA TGTCCAGCCG ATGGGGAAAA CTACTCAAGA CACCTCCGCC TTCAGAGGAG	60 120 180 240 300 420 480 540 600 720
50 55	Nucleic Acid Acci Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATTAGCT ATACAACTCC CCAGAGTAGA TCCACTAGAG TGCACTAGAG GGCCAACTCT TGGTTTCAAA TGTGCAGAGC TCCTCATGCC ATCAATGACT GGATTCAGAC GGCATTCAGAC TCCTCATGCC GGATTCAGTC	ession #: 11 ATTANAGGAC CARACTGACT TACACCAGTT AGGGAGACC AGAGGANAG CTGTGCTCTG ATGGGATCTG ATGTGGATAA GCATTATCCT TTCTCTCTG AGCCCACACA TGCACCTGTG ACCGGAGCC CATCTGCATA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC CTTTGTTGTA ACCAGTTCAC CCAGGAAGCCC ACGCCGGCC ACAGCTGGGT	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGATGA GGAGTTTCTC GGTGCTGCT AGTTCCTGTT AGGAAGTCTGCC CAAGCTGGG CTCCCACGC GCGGACTCTC GCTCCCCCAA AACATACCAT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA TGTCCAGCCG ATGCTCAAGAC CACCTCAGCGC TTCAGAGGAA CACCTCAGCCG TTCAGAGGAC CCAGCACGCA TGGAGACCAC TGGAGACCAC	60 120 180 240 300 360 420 480 540 660 720 780 840
50 55 60	Nucleic Acid Acce Coding sequence 1	ession #: 11 ATTANAGGAC CAMACTGACT TACACCAGTT AGGGAGACC AGGAGACAC CTGTGCTCTG ATGTGGATAA GCATTATCCT TTCTTCCTG AGCCCACACA TGCACCACACA TGCACCTGTG ACCCGCAGCC CATCTGCATA TTCAAACATG	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ACTACCAAAC ATGTGGACAC GGGGAATGAA TCACTGATGA TCACTGATGA ACCAGTTCAC CCAGGAAGCC AGCCCAGCCC	dined sequences of the sequence of the seq	41 41 GAAACTGAGC CCAAAAGTCA GGAAGAAAA GCGATTCTC GGTGCTGCCT AGGAGTGA AGCTGGTT AGGAAGTCGG CCACAGCTGGT CTCCCACCGC GCGGACTCTC GCTGCCCACCGC GCGGACTCTC GCTCCCCAA AACATACCAT TTCAGTGCAG	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA TGTCCAGCCG ATGGGGAAAA CTACTCAAGA CACCTCCCGC TTCAGAGGAG CCAGTCCGAC TGGAGACCCA TGGAGACCCA TGGAGACCCA CCAGTCAGAA	60 120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	Nucleic Acid Acci Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATTAGCT ATACAACTCC CCAGAGTAGA GCCACTAGAG TGCACTAAGA GGCCAACTCT TGGTTTCAAA TGTGCAGAGC TCCTCATGGC ATCAATGACT GGATTCAGTC GCATTCCCTG CTACCCCTCTGCTTTCCCGA	ession #: 11 ATTANAGGAC CANACTGACT TACACCAGTT AGGGAGACCC AAGAGGANAG CTGTGCTCTG ATGTGGATAA GCATTATCCT TTCTCTCTG AGCCCACACA ACACCCACACA TGCACCTGTC CATCTGCATA TCCAACATA CCTGCCATTA CCTGCCATTA CCTGCCTTTA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC CAGGAATGAA ACCAGTTCAG ACCAGGAAGC ACCAGGAAGC ACCAGGAGC ACAGCTGGGT CCGTGTACT CCCTTTAACAA	dined sequences of the	41 { GARACTGAGC CCAAAAGTCA GGAAGAAAC CTGAGGATGA GAGATGGAAT AGCGTTTCTC GGTGCTGCT AGGAGTCG CTCCACCGC CCGGACTCTC GCTCCCCCAA AACATACCAT TTCAGTGCAA AGGCTCTCT TGCTGCTCTC TGCTGCTACTCC TTCAGTCCAC TTCAGTCCAC TTCAGTCCAC TTCAGTCCAC	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG CGCATGGCTA CACCTGACCA TGTCCAGCCG TTCAGGGGAAAA CTACTCAAGA CACCTCCACC TCAGAGGAG CCAGCACCAC TGGAGACCAC TGGAGACCAC TGGAGACCAC CCAGTCACAA CTCGAAGCAC GGAAGTCACAC GGAAGTCACAC	60 120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020
50 55 60	Nucleic Acid Acoc Coding sequence 1	ession #: 11 ATTANAGGAC CARACTGACT TACACCAGTT AGGAGACC ATGGGATAA CCATTATCCTC ATGGATAA GCATTATCCT TTCTCCTG AGCCCACACA AGCCCACACA ACCCCACCACCA ACCCGCAGCC CATCTGCATA ACCACTGTG ACCCGCAGCA CATCACATA ACATCCAATA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAC ATGTAGCAAAC ATGTAGCAAAC ATGTAGCAAAC CTTTGTTGTAGA ACCAGTTCAC CCAGGAAGCC ACAGCTGGGT GATCTGGTTC CCGTGTTACTC CCTTTAACAA TCACAGTGAC	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAA CCTGAGGATGA AGCGTTTCTC GGTGCTGCT AGTACCTGTT AGGAAGTCTG CAAGCTGGGT CTCCCCCAA AACATACCAT TTCAGTGCA AGGCTCTC GCTCCCCAA AACATACCAT TTCAGTGCA AGGCCTCTT TTCAGTGCAACT TTCAGTGCAACT TTCAGTGCAACT TTTAAGCCT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA ATGGGAAAA CTACTCAAGC ATGGGAAAA CTACTCAGAG CCAGCACGC TTCAGAGGAG CCAGTCAGAA CTGAAGCAC CCAGTCAGAA CTGGAAGCAC CAGAAGTGCAC ATGTGAATTC	60 120 180 240 300 360 420 540 600 720 780 840 900 960
50 55 60	Nucleic Acid Acci Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATCTAGCT ATACAACTCC CCAGAGTAGA GCCTAAGAG TGCACTAAGA TGTGCAGAGT TCGTTTCAAA TGTGCAGAGC TCCTCATGCC ATCAATGACT GCATTCACTG CTATCACTG CTACCCTTTTCCCGA AGCATTGAGC AGTGCATTTG TGGAGTTAGC	ession #: 11 ATTAAAGGAC CAAACTGACT TACACCAGTT AGGGAGACCC AAGAGGAAAG CTGTGCTCTG ATGGATATCA TTCTCTCTG AGCCCACACA TGCACCTGTG ACCCGCAGCC CATCTGCATA TCCAACATA CCTGCCTTA CCTGCCTTA CCTGCCTTA ACTCCATTA ACTCCATTA ACTCCATTA ACTCCATTA ACTCCATTA ACTGCCTTCA ACTCCATTA ACTGCCTTCA AAAGGGAACA AAAGGGAACA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTTA AAGTAGAAAA ATGTGGACAC ATGTGGACAC ATGTGGACAC TTTGTTGTGA ACCAGTTCAC CCAGGAAGCC AGCCCAGCCC	dined sequences of the	41 GARACTGAGC CCAAAAGTCA GGAAGAAAC CTGAGGATGA GAGATGGAAT AGCGTTTCTC GGTGCTGCT AGGAAGTCTG CAAGCTGGGT CTCCACCGC GCGGACTCTC GCTCCCCCAA AACATACCAT TTCAGTGCAG AGGCTCTTC TGCTGCAACT TGCTGCAACT TTCATGCAG AGGCTCTTC TGCTGCAACT TACATGCAG AGGCTCTTTC TGAAGGAGCAC ACTACTTACT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGACA TGTCCAGCCG ATGGGGAAAA CTACTCAGCC TTCAGAGGAA CACCTCCGCC TTCAGAGGAG CCAGCACCA TGGAGCAC GGAGCACCA TGGAGCAC GGAGTCAGAA CTGGAAGCAC GGAAGTCACA ATGTGATTGC TGTATGCAAA CTCCAATTGG	60 120 180 240 300 360 420 540 600 6600 720 780 840 900 960 1020 1020 1140 1200
50 55 60	Nucleic Acid Acoc Coding sequence 1	ession #: 11 ATTANAGGAC CANACTGACT TACACCAGTT AGGAGACCC ATGGATAA CCTGTGCTCTG ATGCATAA GCATTATCCT TTCTCCTG AGCCCACACA TGCACCACACA TGCACCTGTG ACCGCAGCC CATCTGCATA ACATCCATA ACATCCATA ACATCCATTA ACATCCATTA ACATCCATTA ACATCCATTA ACATCCATTA ACATCCATTA ACATCCATTA ACATCCATTA ACTCCACTGCATA TTCGACTGCAA TTCGGCCTGA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ATGTGGACAC ATGTGGACAC CTTTGTTGTGA ACCAGTTCAC CCAGGAAGCC ACAGCAGCC ACAGCAGCC ACAGCTGGT GATCTGGTTC CCGTTTACTA TCACAGTGAC CTTTGGCAGT CCTTTGACAA TCACAGTGAC CAGAGAGAC CAGAGAAAAA	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAC GGAGGATGA GGAGTTCTCT GGTGCTGCT AGTTCCTGTT AGGAGTCTG CAAGCTGGGT CTCCCCCAC GCTCCCCCAA AACATACCAT TTCAGTGCAG GGGCTCTTC TTCAGTGCAG GGGCTCTTC TTCAGTGCAG AGGCTCTTC TTCAGTGAACT TTCAGTGCAG AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAGAGGGACGGG	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA TGTCCAGCCG ATGGGGAAAA CTACTCAAGA CACCTCCGCC TTCAGAGGAG CCAGTCAGAA CTCGAACCA TGGAGACCAC CTGAAGCAC CTGAAGCAC ATGTGATGCA ATGTGATTGC TGTATGCAAT CTCAATTGG CGAATGACAC CGGATGAAA CTCCAATTGG CGGTTAGACAC CGGTATGCAAT	60 120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1080 1140
45 50 55 60 65	Nucleic Acid Acci Coding sequence 1	ession #: 11 ATTANAGGAC CARACTGACT TACACCAGTT AGGGAGACCC ATGGATATA ATTGGATAA ACATCACT ATCTCCTG ATGCCACACA AGCCCACACA ACCCCCACACA ACCCCACACA ACCCACTGCA ATCGACCTAA ATCGACTGAA AAGGGAACA TCTGATAAAT ACTGATAAAT ACATCGACTGAA AAGGGAACA ACTGATAAAT ACATCGACGAA ACTGCTGAAAAT ACATCGACAC ACTACACAC	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTTA AAGTAGAAAA ATGTGGACAC GGGGAATGAA TCACGAGAC CCAGGAGCA ACCAGTTCAC CCAGGAGCC ACAGCAGCC ACAGCTGGT CCTTTAACAA TCACAGTTGC CCTTTAACAA TCACAGTGAC CCTTGACAC CCTGAGAGC CAGAGAAAAA CACAGGTCAT ACCAAGTATA	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGATAA AGCGTTTCTC GGTGCTGCT AGGAAGTCTA AGCAGTTGT AGGAAGTCTA AGCAGTCTG CTCCACCGC GCGGACTCTC GCTCCCCAA AACATACCAT TTCAGTGCAG AGGCTCTTC TGCTGCACCAC AGGAGTCTTC TCAGTGCAG AGCATTACTA ACATACCAT AGGACTGCT TACTGCAACT TACTAGCAC AGGCCTCTTC TACTGCAACT TACTAGCAC AACATACTT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGACCA TGTCCAGCCG ATGGGGAAAA CTACTCAAGA CACCTCCGCC TTCAGAGGAG CCAGCACGA TGGAGACCAG CCAGTCAGAA CTCGAAGCAC TGGAGCAC GGAAGTGCAC ATGTGATTGATTGC TGTATGCAAA CTCCAATTGG CGATAGACAC TGTATGCAAA CTCCAATTGG CGATAGACAC TATTCTGGCG TAGCCAAGGA TATTCTGGCG TAGCCAAGGA TATCCTAAGGA	60 120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380
45 50 55 60 65	Nucleic Acid Acci Coding sequence 1	ESSION #: 11 ATTANANGGAC CARACTGACT TACACCAGTT AGGGAGACCC ANGAGGANAG CTTTGGATTA ACATTATCT TTCTCTCTG AGCCACACA TCCACTGTG ACCACTGTG ACCACTGTG ACCACTGTG ACCACTGTG ACCACTGTG ACCACTGTA TCAAACATG ACATCCAATA TCAAACTG ACATCCATTA CCTGCCTTTA GCCACTGCA AAAGGGAACA TCTGATAAAT GACATTGGTG ACATTGCTG ACATTGCTG ACATTGCTG ACATTGCTG ACATTGCTG ACATTGCTG ACATTGCTG ACATTGCTG ACTTTACCACC CGAATTTATG ACGATTGCTG ATGGATGGCA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ATGACAAAC ATGTGGACAC ATGTGGACAC CTTTGTTGTGA ACCAGTTCAC CCAGGAAGCC ACAGCTGGGT GATCTGGTTC CCGTTGACTA TCACAGTGAC TCTTGTGACA TCACAGTGAC CAGGAGACAC ACAGGTGACT CCTTTAACAA TCACAGTGAC CTTGGCAGT CAGGAGAACAA ACAGGTCAT ATCCAATATA ACAGGTGGT ATCCAATATAA AACAGCTGGT	dined sequences of the	41 GARACTGAGC CCAAAGTCA GGAGGATGA GGAGTGGAT AGCGTTTCTC GGTGCTGCT AGGAGTGGT CTCCCGCT AGGACTGGT TTCCCGCT CTCCCCAA AGCATCCC GCTGCTCCCCAA AGCATCCCC AGGACTCTC GCTCCCCAA AGCATCACT TTCAGTGCA AGGCTTCT TGCACACC TTACTACCT AAGGACAC CACTACTTACT AAGGACGG CCACTGGTT AATATTTCTT ACACATACT TCCAAGGCC TCCAAAGGCC TCCAAAGGCC TCCAAGGCC TCCAAAGGCC TCCAAAAGGCC TCCAAAAGCTC TCCAAAGGCC TCCAAAAGCC TCCAAAAGCC TCCAAAACTC TCCAAAGGCC TCCAAAACTC TCCAAAGCC TCCAAACTC TCCAAAACTC TCCAAAGGCC TCCAAACTC TCCAAAACTC TCCAAACTC TCCAAAACTC TCCAAAACTC TCCAAAACTC TCCAAAACTC TCCAAAACTC TCCA	and stop codons) 51 † TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA ATGGGAAAA CTACTCAGCG ATGGGAAAA CTACTCAGCG TCAGAGGAG CCAGTCAGAA CTGAACCA GGAAGTCCA GGAAGTCCA GTATGCAAA CTCCAATTGG CATTCTATGCAAA CTCCAATTGC TGTATCCAATTC TGTATCCAATTC TGTATCCATTGCT TAGCCAAGGA AGTTTTGATTT CTGATGATTAC	60 120 180 240 300 360 420 480 540 600 720 780 900 960 1020 1080 1140 1200 1320
50 55 60 65	Nucleic Acid Acci Coding sequence 1	ession #: 11 ATTANAGGAC CARACTGACT TACACCAGTT AGGAGACCC ATGGATAAC ATGGATAAC ATGGATAA GCATTATCCT TTCTCTCTG AGCCCACACA AGCCACACA ACCGCAGCC CATCTGCATA ACCACTGAA ACCACTGAA ACCACTGAA ACCACTGAAAC ACCACTGAAAC ACCACTGAAAC ACCACTGAAAC ACTGCCTTA ACCACTGCAA ACCACTGAAAC ACTGATAAAA TCGACTGAAAAA TCGACTGAAAAA TCGACTGAAAC ACTGATAAAA TCGACTGAAAAA TCGACTGAAAAA TCGACTGAAAAA TCGACTGAAAAA ACCACTGATAAAA TCGACTGAAAAA ACCACTGATAAAA ACCACTGAAAC ACTGATAAC ACTACGAAC CCTCGGAACC	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ATGTGGACAC GGGGATGAA TCACGAGCA ACCAGTTCAC CCAGGAAGCC ACCAGTTCAC ACCAGTTCAC CCAGGAAGCC ACAGCTGGGT CCCTTTAACAA TCACAGTGAC CCTTGGCAGTT GGGGGACCGA CAGGAGAAAA ACAGGTCAT ATCCAATATA GCAGAAGAAAA AACAGCTGGT TGATCTTAAC	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGATAA AGCGTTTCTC GGTGCTGCTC AGGAAGTCA GGAAGTCA GGAAGTCA GGAAGTCA GGAAGTCA GGAAGTCTG CCACCGC CCGAACTCT GCTCCCCCA AACATACCAT TTACTAGCT TACTAGCAG AGGCTCTTC TACTAGCAC AGGCTCTTC TACTAGCAC AAGGAGAGC CCACCTGGTT AATATTCTT ACACATACTC TCCAAGGGCT CCAAGGGCT CCAAGGGCT CCAAGGGCT CCAAGGGCT CCAAGGGCT CAAGAGCT CCAAGGGCT CCAAGGGCT CCAAGGGCT CCAAGGGCT CAAGACACGT CCAAGGCT CAAGACACGT CCAAGGCT CAAGACACGT CCAAGGCT CAAGACACGT CCAAGGCT CAAGACACGT CCAAAGGCT CAAGACACGT CCAAAGGCT CAAGACACGT CAAACACACC CAAGACACACT CCAAAGGCT CCAAAGGCT CAAACACACC CCAAAGACACCT CCAAAGGCT CACAACACACC CCAAACACACC CCAAAAACACC CCAAAAACACACC CCAAAAACACC CCAAAAACACC CCAAAAACACC CCAAAAACACC CCAAAAACACACC CCAAAAACACC CCAAAAACACACC CCAAAAACACACC CCAAAAACACC CCAAAAACACC CCAAAAACACC CCAAAAACACACACC CCAAAAACACC CCAAAAACACC CCAAAAACACC CCAAAAACACACACACACC CCAAAAACACACACACACACACC CCAAAAACACACACACACACACACACACACACACACACAC	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGACTA CACCTGACCA ATGCGGAAAA CTACTCAAGA CACCTCCGCC TTCAGAGGAG CCAGTCAGAC CCAGTCAGAC CCAGTCAGAC CCAGTCAGAC CTGAAGCAC TGGAAGCAC TGTATGCAAA CTCCAATTGG CGATGCACA TTGTATCCAAT TGTATGCAAA CTCCAATTGG CGATGCACA TGTATTCTGCGG TAGCCAAGGA AGTTTGATTTT CTGATGATAC TCGATGATAC TCGATGATAC TCGATGATAC TCGATGATAC TCGATGATAC TCGATGATAC TCATAGACTA	60 120 180 240 300 360 420 540 600 720 780 900 960 1020 1260 1140 1200 1260 1320 1380 1440 1560
45 50 55 60 65	Nucleic Acid Acoc Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATTAGCT ATACAACTCC CCAGAGTAGAG GCCACTTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGAG TGCACTAGC TATCATAGC TGGATTCCCTG CTATCCCTG CTATCCCTG CTATCCTTG TGGAGAAGTT TTCCAGAT TCTCCTGCTG TGTAAAACTA ACAGCACTCC TATGGATCA ATTCGTGTTA	11 ATTANAGGAC CARACTGACT TACACCAGTT AGGGAGACCC AGAGGAAAA CCTGTGCTCTG ATGGGATACCT TTCTCTCCTG AGCCCACACA TGCACCTGTA ACCACCTGTA ACCACCTGTA ACCACCTGCATA TCCACCTGCATA TCCACCTGCATA TCCACCTGCATA TCCGCCTGA ACTGCCTTA GCCACTGCAA TCTGGCCTGA ACTGGCTGAACC CGTACTGCAC ACTTGCATA TCTGCTTTA GCCACTGCAA TCTGGCCTGAACC CGTACTGCAACC CGGACTTGGTAACC CCTCGGAACC CGGACTTGGT ACTACCAGCA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAC ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC CCAGGAAGCC ACAGCTGGGT GATCTGGTTC CCGTTAACAA TCACAGTGAC CAGAGAGAC ACAGGTGAC CAGAGAGAAAA ACAGGTGAT ATCCAATATA ACCAGTATAA AACAGCTGGT TGAAATAAT	dined sequences of the	41 GARACTGAGC CCAAAAGTCA GGAAGATGA GGAGTGGAT GGAGTTCTCT GGTGCTGCT AGTTCCTGTT AGGAGTCTG CTCCCCAA AACATACCAT TTCAGTGGAT TTCAGTGGAT TTCAGTGCC GCTGCTCCCCAA AGGCTTCTC CAAGGAGAGAG AGGCTCTTC GCTACCCACA AGGCTTCTC CAAGGAGAGAG CCACTGGT AATATTCTT ACACATACT TCCAAGGGCT CCAAGGGCT CCAAGGCT CCAAGGCT CCAAGGACAGTT TCCAAGGCT TTCCAAGGACAGTT TCCAAGGCT TCCAAGGCT TCCAAGGCT TCCAAGGCT TCCAAGGCT TCCAAGGACAGTT TCAACCAATT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA CACCTGACCA ATGGGGAAAA CTACTCAAGCAG CTGCAGCAG CCAGCACGAC TGAGAGCAG CCAGTCAGAA CTCGAACCAG CCAGTCAGAA CTCGAACCAG CAGTGATTCC TGTATGCAAA CTCCAATTAG CTCAATTAG CATTCTGAGCA TATTCTGCG TAGCCAACGA AGTTTTGATTAC TCATAGACTAC TCATA	60 120 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1500 1560 1660 1680
50 55 60 65	Nucleic Acid Acci Coding sequence 1	ession #: 11 ATTANAGGAC CARACTGACT TACACCAGTT AGGAGAACC ATGGATAA AGGATCAC ATGGGATAA GCATTATCCT TTCTCTCTG AGCCCACACA TCCACACA ATCACACA ATCACACA ATCACACA ATCACACA ATCACACA ATCGCTTAA ACATGCACACA ATCGCCTGAACA ATCGCCTGAACA ATCCACC GGAACTTATC ACTCCCC GGAACTTATC ACTCGCAC ACTCGGAACC ACTCGGAACC ACTCGGAACC ACTCGGCAC ACTCGGCAC ACTCGGCAC ACTCTGCCC ACTCGCAC ACTCTGCCC ACTCCGCAC ACTCTGCCC ACTCCGCAC ACTCTGCCC ACTCTGCCC ACTCTCGCC ACTCTCGCC ACTCTCGCC ACTCTCCCC ACTCTCCCC ACTCTCCCC ACTCTCCCC ACTCTCCCC ACTCTCCCC ACTCTCCCC ACTCTCCCC ACTCTCCC ACTCTCCCC ACTCTCCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCCC ACTCTCC ACTCTCCC ACTCTCC ACTCTCC ACTCTCCC ACTCTCC ACTCTC ACTCTCC ACTCTC ACTCT ACTCTC ACTCT	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACAGATTA AAGTAGAAAA ACTAGCAAAC ATTGTGACAC GGGAATGAA CCAGTCAG ACCAGTCAG ACCAGTCAG ACCAGTCAG ACCAGTCAG CCAGGAAGC ACAGCTGGGT CCTTTAACAA TCACAGTGAC CCTTGGATC CCTTGACAA ACAGCGGT ACAGCTGGT TGACAATATA GCAGAAGAAAA ACAGCTGGT TGATCTTAAC ATCCAGTAGT TTGAATATA TCAATATA TAGCAGTGAT TTGAACTAT TTGAAATATT TTGAAATATT	diined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAA CTGAGGATGA GGAGTGGAT AGGGTTCTC AGGAGCTGGT CTCCCCCAA AACATACCAT TTCAGTGCAG GGAGCTGGT TCAGGAGCAGAGAAAA ACATACCAT TTAAGGCTGGT GAAGGAGGAG AGGCTGTT AGGAGGAGGACCTGCCCAA ACATACTAC CAACGAGGACGGC CCACCTGGTT AATATTCTT ACACATACTC TCCAAGGCT GAAGAAAAAGA TCAACCATT	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GCCATGACCA TGTCCAGCCG ATGGGGAAAA CTACTCAAGA CACTCCGCC TTCAGAGGAG CCAGTCACCA TGGAGACCCA TGGAGACCCA TGGAGACCCA TGTATGCAAA CTCCAATTGG CATTTGATTCCAATTGG CATTTGATTCCATTGG CGTATGCAA CTCCAATTGG CGTATGCAA CTCAATTGG CGTATGCAA CTCAATTGG CGTATGCAA CTCAATTGG CGTATGCAA CTCAATTGG CGTATGCAA CTCAATTGG TAGCCAAGGA AGTTTGATT TGTATGATTC TCAATGATTA TGGAGCAAGT TGGAGCAAGT TGGACAAGT TGGAGCAAGT TGGAGCAAAGT TGGAGCAAAGT TGGAGCAAAGT TGCAATGGAAA CTGCATTGC CTCATTGCC TCATGCAATGCA	60 120 180 300 360 420 480 540 660 720 780 900 960 1020 1320 1340 1440 1500 1560 1560 1680 1740
50 55 60 65	Nucleic Acid Acci Coding sequence 1 GACTGCTTGC AGAGATGGAG GGATTAGCT ATACAACTCC CCAGAGTAGA GCCAACTTAGCT TGGTTTCAAA TGTGCAGAGT TGGATTCAGAC TCCTCATGCC ATCAATGAC TCTCATGCT GCATTCCCTG GCATTCCTG CTTTTCCCGA AGCATTGAG AGGATTAGC AGGAAAGTT TTGCAGATT TTGCAGATT TTGCAGATT TTTCCAGATT TTTCAGATT TGAGAGATTT TGAGAGATT TGAGAGATT TGAGAGATT TGAGAGATT CCTCCCGGCAT	11 ATTANAGGAC CARACTGACT TACACCAGTT AGGGAGACCC AGAGGAAAA CCTGTGCTCTG ATGGGATACCT TTCTCTCCTG AGCCCACACA TGCACCTGTA ACCACCTGTA ACCACCTGTA ACCACCTGCATA TCCACCTGCATA TCCACCTGCATA TCCACCTGCATA TCCGCCTGA ACTGCCTTA GCCACTGCAA TCTGGCCTGA ACTGGCTGAACC CGTACTGCAC ACTTGCATA TCTGCTTTA GCCACTGCAA TCTGGCCTGAACC CGTACTGCAACC CGGACTTGGTAACC CCTCGGAACC CGGACTTGGT ACTACCAGCA	NM_014253 65-8242 (under 21 TTCCTCATCC GCAAACCCTA CTTCTGATGA TGCACGAGTA AAGTAGAAAA ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC ATGTGGACAC CCAGGAAGCC ACAGTTCAC CCAGGAAGCC ACAGCTGGGT CCCTTTAACAA TCACAGTAC CCTTGGCAGTT CGGGGACCGA CAGAGAAAAA ACACGTGAT ATCCAATATA GCAGAAGAAAA AACAGCTGGT TGAATCTTACAT ATTCTCATTG TGTGGTGT TTGAAATAAT ATTGTCATTG GGCCAGAGTG	dined sequences of the	41 GAAACTGAGC CCAAAAGTCA GGAAGAAAA GCGATTCTC GGTGCTGGT AGGAGTCTGT AGGAGTCTG CTCCCCCAA AACATCA GCAAGCTCTC CTCCCCCAA AACATACCAT TTCAGTGCA GGAGCTCTC GCTCCCCCAA AGGCTCTCT TAGTAGCAC TACTACT TACTAGCC CAAGGAGAGAC CACTCGTT AAGGAGAGG CCACTGCTT TCAAGGACAGT TTCAAGGACAGTT TCCAAGGCT TCCAAGGCT TTCCAAGGCT TTCCTTGAC TCCAAGGACAGTT TCCAAGGACAGTT TCCAAGGACAGTT TCCAAGGACAGTT TCCAAGGAAAA TCAACCAAT TCCTTGGAC TACGAGAAAA GAAGAAAAAA	and stop codons) 51 TTGCTTAATC AGCATGAAAT CAAGACAGTC ATTACAATAG TCTGTGAAAC GGCATGGCTA TGTCCAGCCG ATGGGGAAAA CACCTCCGCC TTCAGAGGAG CCAGTCCAGCA TGGAGACCAG CCAGTCAGAA CTCGAACCA TGAGACCAC TGAAGCAC TGAAGCAC TGAAGCAC TGAAGCAC TGAAGCAC TTTCTGAACCAC TATTCTGCGA ATTCTGACCA TATTCTGCCA TATTCTGCCA TATTCTGATGATAC TCAATTGATTT CTGATGATTAC TCATAGACTAC TCATAGACTAC TCATAGACTAC TCATAGACTAC TCAATGGAAC TCAATGGAAA CTCAATGGAAA CTCAATGGATAC CCAATGGAAA CTGAACTGTTC GCACTGTTG GCACTGTTG GCATTGATCC	60 120 240 300 360 420 480 540 660 720 780 960 1020 1140 1260 1320 1320 1340 1500 1560 1660 1680

	AGGAGAAATA	TGCGAGGAAG	AGGACTGCCT	AGACCCAATG	TGTTCCAACC	ATGGCATCTG	1980
	TGTAAAAGGA	GAATGTCACT	GTTCTACTGG	CTGGGGAGGA	GTTAACTGTG	AAACACCACT	2040
	TCCTGTATGT	CAAGAGCAGT	GCTCAGGACA	CGGAACTTTT	CTTCTGGACG	CTGGAGTATG	2100
_		CCCAAGTGGA					2160
5		GGAGTCTGCT					2220
		GAACGCTCCT					2280
	AAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
		GATGGCTGCC					2400
10	AAATGGTTGG	CACTGTGTGT	GTCAGGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTCAT	2460
10		TGTGGAGATA					2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCCT	CTCTGCCAGG	GCTCACCAGA	2580
		CTCATTCAGC					2640
		ATCAAATTCC					2700
1.5		AGCAGGCGTG					2760
15		GGAGTGAATG					2820
		GGAAGCTTTG					2880
		CCTTTCCTGC					2940
		AAAGTCACCA					3000
20		AGCCCAAACC					3060
20		AGGGGAACTA					3120
		TTTGTGAGGC					3180
		CTTCTGACAC					3240
		GAAGGGCGAC					3300
25		TGGAACAAGA					3360
_□ 25		GTGGGATATG					3420
- 5 mm		TTACAAGGTT					3480
.ā		ATTTTGAATC					3540
1		CAGCAGCCCC					3600
30		ACCAACTGCA					3660
30		GCCCTGATG					3720
2 2 2		GGAAACTCCG					3780
gF 4		ATGGACCCTG					3840
		TTGAAATCTC					3900
35		GGTGATCAGT					3960
		GCTTCACTGA					4020
gr men		GATGGGACTA					4080
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= 40		GATAACAACA					4260
		CCCATTCACT TCCACTCTAG					4320 4380
or china		GAAACAGACG					4440
F.122		ATCATCGCTG					4500
		TCAGGTGATG					4560
45		TCGCCTGATG					4620
		AGGAACCAAG					4680
r ar li		GAACTGTACC					4740
TO THE PERSON OF		GACTATGTTT					4800
		AATGGCAATT					4860
50		CCTGGCGGAC					4920
		GCCCAAGGCT					4980
	TCTGGCTACC	AAAAGTAACG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCCGAGGG	5040
	ACACCTGACC	AATGCAACGT	TTCCCACTGG	AGAGGTCAGC	AGCTTCCACA	GTGACCTGGA	5100
~ ~	GAAGCTGACA	AAAGTGGAGC	TAGATACTTC	CAACCGTGAA	AATGTCCTCA	TGTCAACCAA	5160
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	GGTGAATCCA	GATGGTTCCC	TGCGTGTCAC	TTTTGCCAGC	GGGATGGAGA	TCGGCCTCAG	5280
	CTCAGAGCCC	CACATCCTGG	CAGGGGCAGT	CAACCCTACC	CTGGGCAAAT	GCAACATCTC	5340
		GAGCACAATG					5400
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OU		CATATAACCC					5520
		TATGACCAGA					5580
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		AGCTTACAAA					5880
		AGCACTTCTT					5940
		GGGACAGGGC					6000
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70							6120
		GGACGCCAGA					6180
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		ATTAATTACG					6300 6360
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		ATGACCATTC					6480
		GATGCCAATA					6540
		TCTGTAAATG					6600
_		TTAAGCCATG					6660
80						GCTTTCTGAG	

		AATGATATT					6/80
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		CTAGGGCAGC					6900
-		TTGTACAACC					6960
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	TACAGGTACC	CCACTAGCTG	TGTTCAGCAG	CCGAGGTCAG	GTCATAAAGG	AGATACTATA	7080
		GGCGATATCT					7140
	TCATGGAGGA	CTCTATGATT	TCCTTACTAA	ATTAGTGCAC	CTGGGGCAAA	GGGATTATGA	7200
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10		TTCAACCTCT					7320
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		TATACCACAG					7380
	CAATGTACTA	CCTGGATTTC	CCAAACCTGA	ATTAGAAAAT	TTAGAATTAA	CTTACGAGCT	7440
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							7560
15		CAGAAACAGC					
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	TTCTGTTTTT	GGGAAAGGTA	TAAAATTTGC	CATCAAGGAT	GGCATAGTAA	CAGCTGATAT	7680
		GCCAATGAAG					7740
		CTACATTTTA					7800
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	CCANANCCAC	CAGCTTTTGA	GCACTGGGGGG	CCTACAACCT	ТАССАТСССТ	ጀ ብብብ ነገር መስመተ	8160
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		CAGTATTTAG					8220
- 122.		GGCAGGAGGT					8280
aCi	GTTTTTAAAA	CATAAAATGG	TTTATTGTAT	TGGTTTTCTA	GATCAGAACT	CTGTATATGT	8340
To ACTO		GAAAAACATA					8400
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్ిం∩		TAAACTCTTT					8460
30	CAAAATAACA	CAAGTAGAAC	TCAAACAGCT	AAAAACAGTT	TTCAGAAAGC	ACCACTTTCA	8520
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M		CAGTTTCATC					8640
(5		ATCTGAAACT					8700
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35	AGGACCCAAT	TGCCCTTCCT	TCTTGATTAT	TCCTCCTTGC	TTGTTAAAGT	AAATGCCATA	8820
		GTGTTTTGGC					8880
£ ,28.		AGACTGTATA					8940
Ę	GCCAGCGTGA	CCTCTCTCAC	ACGACCTGTT	TTGACTCAAT	TTTTTACTAA	AAGTTGTTCA	9000
	GCTGTATTGG	TATCATGTAA	ACATAGCTTT	TATTAACCTG	GGTAGGAATT	TCTCATTTAT	9060
= 40		TGTTTTGGTC					9120
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		TGCACATGAA					9180
G:000	ACAAAGGCTT	TAGCAGGCAT	ACGTGTCTGG	GATGCCGATA	CATACATTAA	CTACTACTGC	9240
	AGAAATTCAT	AAGAGCCAAA	ACCTTAAAAA	AATAGACCTG	GTACTTAAGT	GAAAGTACTA	9300
	AAGGGAAGAC	CAGACCAAAC	ATCACAGCAG	TTGCTGCCAC	ATTGTTTCAG	CCCACTTAGA	9360
45		AAATGTACAA					9420
12		TCCTTTCCAA					9480
ran ^g	TTTACTAAAA	TAATTTATAC	AGTTAGTTAT	TTTCGTTCTC	CGTACTTACC	CATTTATCTT	9540
		TCTCTACTGC					9600
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	TGACAAAGAG	ATAGTTTGTA	AAATGCTGTG	TAATTGTAAG	TTACCACAAA	TGAAAATACA	9780
	TCACACCACA	ATGTGGCCCG	TACAAAATTC	CCCTGAGCCA	COMMONGOR	መመጥር አመር አርርር	9840
		ATTTGCTATG					9900
~ ~	TTCCAGATGC	TACCTAAATG	CAGTGTGGGG	TCATTGCCTT	GCTTTGCGAT	GACAGTTTCT	9960
55	TTGAAAATAT	GCAAAGTCAT	AAGCTCATGT	TAAGGTTTTT	CAAGAGTCTG	CCTCCTACTA	10020
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		TTTCAAAACC					
	AGAATTCATG	AGGAACTCAT	CTCTCTTTAT	AACTGGAAAC	ACACCAGCTT	GATATATTGC	10200
	TAATCCATAC	TAAAATCATA	ጥተልጥተርርርጥተ	ጥተጥጥጥርልልጥ	CACCCCTCTA	ጥጥልልጥርርጥልሮ	10260
60							
00		CAGAATGGAA					
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	ATGGAAAAAT	AATTTGTGAA	CTGTATATAG	AGAGTGCATT	CATAAATGTG	ATTATGTATT	10440
	ΤΤΑΤCΑCΑΑΑ	TCCAAAATGT	САВТАТТАСА	CHALLALAGO	ርጥተንፈጥልተተጥተ	አ ልርር አልጥተልጥ	10500
		AATTCATTGA					
65							
U.S		GAAGCTTTTA					
	AATACGTATT	TGGTTGGTTC	GTGCCTTTAG	TTTGTTAAAG	TTACATTTGT	ATTATATTCA	10680
		TTTTTATTAC					
		ACTCCTAAAG					
70		GAAGAGAAAC					
70	TATCACTTCC	TATTCAGCTG	AATAGAAAGA	ATGCCTTCAT	TGACTTGCAG	TTCTGCAGTT	10920
-		AAAGAACAAT					
		AATTTCTCAT					
		GTTAAAGTGA					
	CTGGAGGCAG	GGAATACTCC	ATGGTTGTTT	CTTTTTCCTA	CTTAAGCCCA	TTTTGTTTGT	11160
75		TTTGTTTTGT					
		AGTTTAACAC					
		GCATGACTCC					
	AACAAAACAC	TTTTACCATA	TAAATAAGTA	TATGATTTAT	TTTTAACCCA	AAAAATGTAT	11400
		TGTCCTTTAC					
80							
50	ATATATATA	TATACAACAT	AGCCAAATGT	ATGAAAACTT	GACAATGTAT	AATTTGGAAT	11520

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         АААААААААС АААААААССС СААААААСАА АААААСАААА ААААССАААС ТААААТТТАА 12060
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  15
         AAGCATCAGT AAGAAAGAAG GCGAAAAAGA GAAGTATAGC CTTTATGTCA GAAAAACATT 12480
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CAGTTTCTGT ATAACAACAG GTAGAGGTTC TAATCATATT GAAAATTGTG TTATAATGGT 12600
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  20
         ATTTTGCTCT GGCTTTCAGG CCAGAAGCAT GCATTTTTCT ACAAGAGCAT CACAACAACA 12780
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         TATTTCATTT TTAAAAAATA AAATTGCCAA TGAAAAAAAA
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         SEQ ID NO:230 PEZ2 Protein sequence:
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         Protein Accession #:
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         MEQTDCKPYQ PLPKVKHEMD LAYTSSSDES EDGRKPRQSY NSRETLHEYN QELRMNYNSQ
                                                                                60
          SRKRKEVEKS TOEMEFCETS HTLCSGYOTD MHSVSRHGYO LEMGSDVDTE TEGAASPDHA
                                                                               120
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         LRMWIRGMKS EHSSCLSSRA NSALSLTDTD HERKSDGENG FKFSPVCCDM EAQAGSTQDV
                                                                                180
35
          QSSPHNQFTF RPLPPPPPPP HACTCARKPP PAADSLQRRS MTTRSQPSPA APAPPTSTQD
                                                                                240
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          SVHLHNSWVL NSNIPLETRH SLFKHGSGSS AIFSAASQNY PLTSNTVYSP PPRPLPRSTF
          SRPAFTFNKP YRCCNWKCTA LSATAITVTL ALLLAYVIAV HLFGLTWQLQ PVEGELYANG
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          VSKGNRGTES MDTTYSPIGG KVSDKSEKKV FQKGRAIDTG EVDIGAQVMQ TIPPGLFWRF
                                                                                420
          OITIHHPIYL KFNISLAKDS LLGIYGRRNI PPTHTQFDFV KLMDGKQLVK QDSKGSDDTQ
                                                                                480
          HSPRNLILTS LQETGFIEYM DQGPWYLAFY NDGKKMEQVF VLTTAIEIMD DCSTNCNGNG
                                                                                540
40
          ECISGHCHCF PGFLGPDCAR DSCPVLCGGN GEYEKGHCVC RHGWKGPECD VPEEQCIDPT
                                                                                600
O
          CFGHGTCIMG VCICVPGYKG EICEEEDCLD PMCSNHGICV KGECHCSTGW GGVNCETPLP
          VCQEQCSGHG TFLLDAGVCS CDPKWTGSDC STELCTMECG SHGVCSRGIC QCEEGWVGPT
                                                                                720
}_
          CEERSCHSHC TEHGQCKDGK CECSPGWEGD HCTIAHYLDA VRDGCPGLCF GNGRCTLDQN
                                                                                780
45
          GWHCVCQVGW SGTGCNVVME MLCGDNLDND GDGLTDCVDP DCCQQSNCYI SPLCQGSPDP
                                                                                840
          LDLIQQSQTL FSQHTSRLFY DRIKFLIGKD STHVIPPEVS FDSRRACVIR GQVVAIDGTP
                                                                                900
          LVGVNVSFLH HSDYGFTISR QDGSFDLVAI GGISVILIFD RSPFLPEKRT LWLPWNQFIV
          VEKVTMQRVV SDPPSCDISN FISPNPIVLP SPLTSFGGSC PERGTIVPEL QVVQEEIPIP
                                                                               1020
1.
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                                                                               1080
          FAWNKTDIYG QKVWGLAEAL VSVGYEYETC PDFILWEQRT VVLQGFEMDA SNLGDWSLNK
HHILNPQSGI IHKGNGENMF ISQQPPVIST IMGNGHQRSV ACTNCNGPAH NNKLFAPVAL
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   50
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          YKLKSLVETK DLSKNFEVVA GTGDQCLPFD QSHCGDGGRA SEASLNSPRG ITVDRHGFIY
          FVDGTMIRKI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLEWPTDL AVNPMDNSLY
                                                                               1380
   55
          VLDNNIVLQI SENRRVRIIA GRPIHCQVPG IDHFLVSKVA IHSTLESARA ISVSHSGLLF
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          IAETDERKVN RIQOVTTNGE IYIIAGAPTD CDCKIDPNCD CFSGDGGYAK DAKMKAPSSL
                                                                               1500
          AVSPDGTLYV ADLGNVRIRT ISRNQAHLND MNIYEIASPA DQELYQFTVN GTHLHTLNLI
                                                                               1560
          TRDYVYNFTY NSEGDLGAIT SSNGNSVHIR RDAGGMPLWL VVPGGQVYWL TISSNGVLKR
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                                                                               1920
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          RHSLQTMLSV GYYRNIYTPP DSSTSFIQDY SRDGRLLQTL HLGTGRRVLY KYTKQARLSE
                                                                               1980
          VLYDTTQVTL TYEESSGVIK TIHLMHDGFI CTIRYRQTGP LIGRQIFRFS EEGLVNARFD
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                                                                               2040
          YSYNNFRVTS MOAVINETPL PIDLYRYVDV SGRTEQFGKF SVINYDLNQV ITTTVMKHTK
                                                                               2100
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                                                                               2160
          TVSVNDKTQW RYSYDLNGDI NLLSHGKSAR LTPLRYDLRD RITRLGEIQY KMDEDGFLRQ
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                                                                               2400
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           RLQTKTQEWD PGKTILGIQC ELQKQLRNFI SLDQLPMTPR YNDGRCLEGG KQPRFAAVPS
           VFGKGIKFAI KDGIVTADII GVANEDSRRL AAILNNAHYL ENLHFTIEGR DTHYFIKLGS
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           LEEDLVLIGN TGGRRILENG VNVTVSQMTS LLNGRTRRFA DIQLQHGALC FNIRYGTTVE
                                                                               2640
           EEKNHVLEIA RORAVAQAWT KEQRRLQEGE EGIRAWTEGE KQQLLSTGRV QGYDGYFVLS
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           VEOYLELSDS ANNIHFMRQS EIGRR
                                                     SEQ ID NO:231 PFD4 DNA SEQUENCE:
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Coding sequence:

225-2567 (underlined sequences correspond to start and stop codons)

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	TAGGATCGGT	AATAAAACGT	CCCACTCCCT	TCTGAGAGCG	CTATAAAGGC	AGCGGAAGGG	180
	TACTCCCCCC	GGCATTCCGG	GCGGGGCGCG	AGCAGAGACA	GGTCATGGCA	GCGCCAGGCG	240
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	TGCGGGAGAG	CCTGGCCAAG	TGCTGCAGTT	GTTCAAGAAA	GAGAGCCTTT	GGTGTGCTAA	420 480
	AGACTCTTGT	GCCCATCTTG TTCGGGAGTT	GAGTGGCTCC	CCAAATACCG	AGTCAAGGAA GCTGCAAGGG	ATGGCIGCIIA	540
15	CCCMACTACC	TGCAGTTCCT	CTCCCATATC	GTCTCTACTC	TGCTTTTTTC	CCTATCCTGA	600
1.5	ጥልጥምንልጥልን	CTTTGGAACA	TCAAGACATA	TCTCAGTTGG	ACCTTTTCCA	GTGGTGAGTT	660
	THE ATTROPPORTED	ልጥርግጥርግጥፕ ረር ግጥ	CTGAGCATGG	CCCCCGACGA	ACACTTTCTC	GTATCCAGCA	720
	CCAATGGAAC	TGTATTAAAT	ACTACTATGA	TAGACACTGC	AGCTAGAGAT	ACAGCTAGAG	780 840
20	TCCTGATTGC	CAGTGCCCTG ATTCATAGTG	ACTCTGCTGG	TTGGAATTAT	ACAGTTGATA	TTTGGTGGCT	900
20	TGCAGATTGG	CCAAGTGCTG	CTCTCACACA	TAAACATTCT	CCTCAATGTT	TCAACCAAAA	960
	ACTACAATGG	AGTTCTCTCT	ATTATCTATA	CGCTGGTTGA	GATTTTTCAA	AATATIGGIG	1020
	አጥአ ርር አልጥርጥ	ጥርርጥርልጥጥር	ACTGCTGGAT	TGCTCACCAT	TGTCGTCTGT	ATGGCAGTTA	1080
	አርርኔ አጥጥ እ እ እ	ጥርልጥርርርጥጥን	AGACACAAAA	TCCCAGTCCC	TATTCCTATA	GAAGTAATTG	1140
25 يستر	THE ACCOUNTS AT	ጥርርጥልርጥርር	ATTTCATATG	GAGCCAACCT	GGAAAAAAAT	TACAATGCTG	1200 1260
hed —	GCATTGTTAA	ATCCATCCCA GCTGGCTGCA	AGGGGGTTTT	TGCCTCCTGA	ACTICCACCI CCCTTATCCT	ATTCCACTCT	1320
1Ī	TCTCGGAGAT	AGTATATGCC	ACCARCTATC	ATTACACCAT	CGATGGGAAC	CAGGAATTCA	1380
1000. 13. 1. 1. 1.	ጥጥርርርርጥጥጥርር	CATCAGCAAC	ATCTTCTCAG	GATTCTTCTC	TTGTTTTGTG	GCCACCACTG	1440
30	CHCHTHCCCG	CACGGCCGTC	CAGGAGAGCA	CTGGAGGAAA	GACACAGGTT	GCTGGCATCA	1500
-#-	ጥርጥርጥርርጥርር	CATTGTGATG	ATCGCCATTC	TTGCCCTGGG	GAAGCTTCTG	GAACCCTTGC	1560
	AGAAGTCGGT	CTTGGCAGCT	GTTGTAATTG	CCAACCTGAA	AGGGATGTTT	ATGCAGCTGT	1620 1680
10	GTGACATTCC	TCGTCTGTGG	AGACAGAATA	AGATTGATGC	ACCUCCCCCTT	ATATTTACGT	1740
35	GTATAGTGTC	CATCATTCTG	COUNCYCOUR	CTTCTTCCAA	TGGCCTTGGA	AGCATCCCTA	1800
.⊓35	CCACACATAT	CTACAAAAGT	ACCAAGAATT	ACAAAAACAT	TGAAGAACCT	CAAGGAGTGA	1860
13	ልርልጥጥርጥጥልር	ATTITUTE ACT	CCTATTTTCT	ATGGCAATGT	CGATGGTTTT	AAAAAATGTA	1920
e.	ጥሮ አ አርጥሮሮ አር	እርጥጥርር እ ጥጥጥ	GATGCCATTA	GAGTATATAA	TAAGAGGCTG	AAAGCGCTGA	1980
: . 4O	GGAAAATACA	GAAACTAATA	AAAAGTGGAC	AATTAAGAGC	AACAAAGAAT	GGCATCATAA	2040 2100
40	GTGATGCTGT	TTCAACAAAT	AATGCTTTTG	AGCCTGATGA	TOTO A CONTROL	GATCTGGAGG GAGCTTCCAG	2160
3 22	AACTIGATAT	CCTTCCCAAC	GAAATAGAGA	ATAGCCTTGT	GCTTGACTGT	GGAGCTATAT	2220
L	ር የተመጥጥር ር መር ር ል	COMPONERS	CTCACATCAC	TGCGGGTGAT	TGTCAAAGAA	TTCCAAAGAA	2280
	ጥጥር አጥርጥር አ አ	ጥርጥርጥልጥጥጥ	GCATCACTTC	AAGATTATGT	'GATAGAAAAG	CTGGAGCAAT	2340
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F 1277	ACCTOTOTAT	GAGCAAGGAA	TACAAGACAA	AACTTCCTCA	ATGCATTGAC	TATTTCTTCA	2640
50	CACTCAAAAC	' ልርጣና ልጥጥና ነጥ ነ	מדירבידיטידיידיים י	AGCCATTGAA	AGAGAAGCAC	TAAGACTGCT	2700
	TCTAGGCTTT	AAAATATTA T	TAAACACCTT	ATCCCTAACA	TGGGCAAAAT	GGCTAGAATT	2760
	ATTCAGACGA	TTTGGCAGCG	TCCAGGGTAA	GCTGGTGTTA	TAATACGCTG	CTGATCTACA	2820 2880
	TCACAGATTI	CTAATAAT	TICACGIGG	CACTCACGA	TCICIGITOR	GTTAGAGTGA TAAAGAAAAA	2940
55	ጥር ልርብጣጥጥር	ACTGACCTGG	ATATCCATGA	GCTGCACTGA	TCACCATGT?	AGGTCACATT	3000
00	ጥል ርጥልልልጥርር	TGAAATAAA	TGATTAATGO	: ATTTATCAAT	' AAAAGCCTTI	GAAAATACTT	3060
	ጥርር አጥል አጥል ፤	ATTICGACTITY	TAAAAATGCA	AATTTGCTT	GTATCTAATA	A ATGAAGTGTT	3120
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00	ል እ ል ል ል ጥ ል ጥ ል ጥ ል ጥ	P GACAGATTAT	AATTTOTOTO 1	AATGCAGTT	r Taattatct	r AGTCTATAGA	3360
	AATGATCATT	r GCATGGAGG	: ATGTATAGGT	ATGATCTGT(TAAAATCTG	A CATAAAAACA	3420
	GTGCTATTC	r gagtgaaaa:	TTTTTTGATC	TGCTTACATA	A ACCATGGTG	A TTAAAATGAG	3480
65	ሚሚያቸው ተመመመው የ	r TTCTCAAAA	A TTTTAGCAGT	T GTGTAAAGT	A AGTAATCTT	r AACTGAACTC	3540 3600
03	TGACCACTT	TAAAAAAAA A	TAAAAATTGA	A ACTACCTATA	A GTAGTCTGT	TTTAAAGTGA TGGAATGTAC	3660
	ATTITITAMA	ACAAAGCAI.	r TTTTGACCA	AAGTTTTTA	ATCTTTTCT	TTTATTTATT	
	עיזייראואוארוערעיע (A CTCCCAACA	A THTTCTAGAS	r ATTATATAC	A ACACAGGCT	r TGATCTTGGG	3780
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80	CGTGCCAA	G CACTCCAGC	TGGGCGAAAC	G AGCAAGACT	C CGTCTCAAA	A AAAAAAAAA	4500
30	CGIGCCACI	- Chorconde					

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         AAAGGAAATA TGCACTGCTC ACTTTTTTGA AGGAAATGCC AAAGTTACGT TTTACAACAA
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                                             31
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                                                                                  180
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2
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                                                                                  720
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          ODEAMRTLAS
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(Ö
                                                      SEO ID NO:233 PFH2 DNA SEQUENCE:
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35
          Nucleic Acid Accession #:
                                        228-1097 (underlined sequences correspond to start and stop codons)
          Coding sequence:
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                                              31
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= 40
                                                                                    60
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          TGCTCCTGCT CTTGGTGCAG CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC
j.d.
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                                                                                   240
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[]
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                                                                                   420
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i salar
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                                                          41
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				ATGACTTATG			120
				CAAAACAAAG TGGATTGGAA			180 240
10	TGGGTCTGGG	TAGGAACCCA	${\tt GAAACCTCTG}$	ACAGAAGAAG	CCAAGAACTG	GGCTCCAGGT	300
10						GAGAGAAAAA ATGCTACACA	360 420
				CACGGTGAAT			480
				GGACTCAAGT			540
15				CTGGTTTGCA		GGGAAACTTC	600 660
				AGTGCTCCTA			720
				GGGTTCGTGG GACTGTGAAG			780 840
				AATTGGGACA			900
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				TCCAACCCCG			1140
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[25						GTGGGACAAC GAAGGGTTTG	1320
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1 1 1 1 1 1						TCAGGGACAA	1440 1500
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H	CCTGAAGGAT	GGACGCTCAA	TGGCTCTGCA	GCTCGGACAT	GTGGAGCCAC	AGGACACTGG	1620
1,3 1 .c.=						GGTAGCTGGA GCTTCGGAAA	
(0				GCCAGCAGCT			1800
35		AAAAGCCTTC					
(I							
40	Protein Accession	ACC5 Protein sea n #:	<u>ience:</u> NP_000441				
# 40 []							
	1	11	21	31	41	51	
45	MIASQFLSAL	TLVLLIKESG	AWSYNTSTEA	MTYDEASAYC	QQRYTHLVAI	ONKEEIEYLN	60
A Second						CVEIYIKREK	120
in party.				HGECVETINN DRGYLPSSME		SAPIPACNVV	180 240
	ECDAVTNPAN	GFVECFQNPG	SFPWNTTCTF	DCEEGFELMG	AQSLQCTSSG	NWDNEKPTCK	300
50				CNFTCEEGFM GSSCEFSCEQ			360 420
				FTYKSSCAFS			480
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60	Nucleic Acid Acco	E	1-3793 (under	SEC	2 ID NO:237 PM2	B DNA SEQUENCE and stop codons)	
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65 70	Nucleic Acid Acc Coding sequence 1 ATGATGTGTG GAAAGGAGTG GAAAGGACTTC CTGCCACAGG CCGGAATTTG GAAGAAGAAA TTGGAGTGCC GCCCAGTCTC TTTGAGCACC AGAGTCTCTG AGAGTCTCTG	11	1-3793 (under 21 CACGATTAAT AGACTCCCAT CACCCTTCGG CTATGACCGA ACTACAGGA AAAAGATTAA ACATGAAAGA ATCCAGTGAA AGATGAAAAG AGAACTAGCT AAGAAAAATG AGAAAAATG	ined sequences of 31 GAGGACACCC TTTGAGCAGC GACTCACTCC GAGGACCTGCA AGAACACA TCACTAAGAA TCACTAAGAA GTTGAAGTGC GTTAAGGAGC GCTGCTAATC GCATCAAGCC GCTCAAGCC	DID NO:237 PM20 orrespond to start 41 CAATGAGCCA TGATGGTGAA AAAGCCTCTC AGAGACAGCT GTTCTAAGGG GGGAACAACT CAAGACTATT TGACGGTGGT TCAAGGCACT GACTGAGGTAA AGGAACTGT AGGAGATTGT AGGGAACTACT AGGAGATTGT AGGGAACTACT AGGAGATTCT	B DNA SEQUENCE and stop codons) 51 AAGGGGGTCC TATGCTAGAT ACTTGCCAG CAATTCAGCC GGCTGATCCA TCTAGAAAAG ACTGGAGCAT AAAACGGCAA GAAATCTTTG TTCTTTAGAA TGCCTTGCGT TGCTTCGAA	60 120 180 240 300 420 480 540 600 600 720
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65 70	Nucleic Acid Acc Coding sequence 1 	11	1-3793 (under 21 CACGATTAAT AGACTCCAT CACCCTTCGG CTATGACCGA ACAGGAATTA TAAAGCTGAA ACATGAAAGA ATCCAGTGAA ACATGAAAGG ATCAGTGAA AGAACTAGCT AAGAAAATG AGAACTAGCT AAGAAAATG AGAACTAAATG AGAACTAAATA AGAACAAATA AGAACAAATA AGAACAATA	SEC dined sequences of the sequence of th	2 ID NO:237 PM20 orrespond to start 41 CAATGAGCCA TGATGGTGAC AGAGCACACT GTTCTAAGGG GGGACACACT TGACGGTGGT TCAAGGCACT TCAAGGCACT TCAAGGCACT ACT GACTGAGGT AGAGGATTGT AGGGATTCAC AGAGTTTGTC AGCGTTTGTC TCACGATTCCCC TTTCTTCCCC	B DNA SEQUENCE and stop codons) 51 AAGGGGGTCC TATGCTAGAT ACTTGCCAG CAATTCAGCC GGCTGATCCA TCTAGAAAAGC ACTGGAGCAT AAAACGCAA GAAATCTTTG TCTTTTAGAA TGCCTTGCGT AGAGTCAGA CAATGGTTCT TGAAAAGCAA AGTGGAGCAA GATGGAGCAA GATGGAGCAA GATGGAGCAA AGTGGAGCAA	60 120 180 240 300 360 480 540 600 660 720 780 840
65 70 75	Nucleic Acid According sequences 1	11	1-3793 (under 21 CACGATTAAT AGACTCCCAT CACCCTTCGG CTATGACCGA AAAAGAATTA ACATGAAAGA ATCCAGTGAA ACATGAAAAGA ATCCAGTGAA AGAAAAATG AGAAAAATG TGGACAGAAA TAGTCAAATA TAGTCAAATA AGAAAGAACGT AGAAAAAAG	ined sequences of the sequence of the sequ	OID NO:237 PM20 orrespond to start 41 CAATGAGCCA TGATGGTGAA AAAGCCTCTC AGAGACAACT CAAGACTATT TGACGGTGGT TCAAGGCACT TCAAGGCACT GACTGAGGT AGGAATTGT AAGGATTGT AAGGATTGT AAGGATTGT AAGAATTGCT TATCTTCCCC TATCTTCTCCCAAAACAAGAA	B DNA SEQUENCE and stop codons) 51 AGGGGGGTCC TATGCTAGAT ACTTGCCAG CAATTCAGCC GGCTGATCCA TCTAGAAAAG ACTGGAGCAT AAAACGCCAA GAAATCTTTG TTCTTTAGAA TGCCTTGCGT TGAAAAGCAA CAATGGTTCT TGAAAAGCAA AAATGGTTCT TGAAAAGCAA AATGAAAACACA	60 120 180 240 300 420 420 600 660 720 840 900
65 70	Nucleic Acid Acc. Coding sequence 1	11	1-3793 (under 21 CACGATTAAT AGACTCCAT CACCCTTCGG CTATGACAGGA ACATGAAAGA ACATGAAAGA ATCCAGTGAA AGAACTAGCT AAGAAAATA TAGACAGAAAATA AGAAAAATA TAGAAAAATA TAGAAAAAAT TAGAAAAAT GAAAAAAT GAAAAAAT GAAAAAAT GAAAAAAT GAAAAAAAG GGAGGCATG	ined sequences of the sequence of the sequ	2 ID NO:237 PM20 orrespond to start 41 CAATGAGCCA TGATGGTGAA AAAGCCTCTC AGAGACAACT GTTCTAAGGG GGGAACAACT TCAAGGCTGTT TCAAGGCTGTT TCAAGGCACT AGAGTTGT AGGAGTTGT AGGAGTTCT AAGAATTGT AAGAATTGCT TTTCTTCCCG AACAGAAGA AAGATATGGA	B DNA SEQUENCE and stop codons) 51 AAGGGGGTCC TATGCTAGAT ACTTGCCAG CAATTCAGCC GGCTGATCCA TCTAGAAAAGC ACTGGAGCAT AAAACGCAA GAAATCTTTG TCTTTTAGAA TGCCTTGCGT AGAGTCAGA CAATGGTTCT TGAAAAGCAA AGTGGAGCAA GATGGAGCAA GATGGAGCAA GATGGAGCAA AGTGGAGCAA	60 120 120 240 300 420 480 540 660 720 840 900 900 1020

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           GAACTGGTTT TGAAGAGACA CTCTGAAATG ATAAAGACAG CCTTTAATCC CCCTCCTCMC 1980
           CAGAAGGAAC CTCAAAAGGT AGATGAGGTA CAAGGTCCTA AGTGATCTCT TTTTCTGAGC 2040
           AGGATATCAG GTTAAAAAAA AAAAGTTACT GGCTGGTTTA ATACTTTCTA CCTTCTTCAC 2100
           AGAGCAGCCT TTGAATAGAC TATGTCCTAG TGAAGACATC AACCTCCGCC TTAAGCTATG 2160
           TATGTATGGA GGCCAGTCGC AGCTTTATTA TGCAGACACA CAAGTGGTCT GGACATGAGG 2220
   80
           GTACAGTTTC TGCCTACCAA GACACTACTT GCACTGGATC TTACGCAAAA AAGAACCAGA 2280
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ACACAGTG TGGACAACTG CCCATATATT CTATCTAGAT TAGGAGAGGG TCCTGGCTAG 2340 GATTITAGTG GTAATTCCTA GTTACATTCA ACAAGTATAA AGATTATAGA GCTTATTITA 2400 TGAACTATAA ACTATAATTT AATGCAAAAT ATCCTTTTAT GAATTTCATG TTAATATTGT 2460 GAAATATTAA AATAATTCCR CAATAGTTGA GAAAAATGAG CATTTTTTTC CATTTTTAAA 2520 5 AAATGCATAG AAAAGACAAT TTTAAAATCC TGGGACCATA TTTATTTAGA AGTAGCTGTT 2580
AGTAAAACAT TAGAAAAGGA GTCAGGCCAT TAGGTTATTT ATCCAAATCT CTAAGCAATT 2640
AGGTTGAAGT TATTAAGTCA AGCCTAGAAA AGCTGCCTCC TTGTAAGGCT TTCATGACAA 2700
TGTATAGTAA TCCACAGTGT CCAATTCTTC ACACTCCTCA GGAATATCAC TACCTCAGGT 2760
TACGGTACAC AGGCTATAAT TGATGATGAT GTTCAGATAA CTGAAGACAC AATAAATGAC 2820 10 ATTCAGACAT CAGGAMAAWW CCCTCATGTT CTTTTCTATG ATGGCCACCT GTACCAGCAA 2880 CGTGGGTTTC ACCCACACAA CGATGAACTG TTCTCTTACT TCTCCAGTTG ATTTTAAAGA 2940 CTTGTTAAGA GGTCTTACTA ATAAAATTTG GGTATGATAG AAAAWCCACA ATCAAAWCTT 3000 GAACCAAATA ACATATTAAA TTACTAATAT TTAAGTGATG GAAGACACA AAAAAACTTA 3060 AAAGCACGAA CAACCTAACT TGAAAAAGAA TTTTAAAATA TGATTAACCT GAAGAAAAGA 3120 15 GAATCCTAAG AGCCAAAGCT CCTTTTTATT TAGCTTGGAA TTTTCCTATT GGTTCCTAAC 3180 AAACTGTCCC AATGTCATAT AAGGAAACAT GATCTATTAC ATTCCTTTAT AACAATGTGG 3240 AGAGACTATA AACCATGTA AGTAGTAAAA CTATATYAGA GACTCAGGAG ACTGACTAAA 3300
AGGCCTGGAT CTGCAGTGTA TTATCTGTAT AAAAATTGGC AGGGGGAAGC TAAAAGGAAA 3360
GGAGATTGGA GATCTCAATT CTATCATGGT GTATTTCATA CGCAAATCAG AGCATGCATT 3420
GTTTTTTGTT TTTGGAAAGA GAAGGGAAGT GTGTTCTGCC CCATGTTTCC TTCCGTGTTT 3480 20 ATAGTTCAAA CTCTATATAT ACTTCAGGTA TTTTTTGTTT AGCCCTTCAT TATAAATGGG 3540 CAGGAAATTG TTTATCAACC TAGCCAGTTT ATTACTAGTG ACCTTGACTT CAGTATCTTG 3600 AGCATTCTTT TATATTTTTC TTTTATTATC CTGAGTCTGT AACTAAACAA TTTTGTCTTC 3660 AAATTTTTAT CCAATATCCA TTGCACCACA CCAAATCAAG CTTCTTGATT TTCAAAAAATA 3720
AAAAGGGGGA AATACTTACA ACTTGTACAT ATATATTCAC AGTTTTTATT TATAAAAAAA 3780
ATTTACAGTA CTTATGGAGA GCCAGCAGAA GACATCAGAG CACTCACTTC TTCCCATCTT 3840
TGTTAAGGTT AGCGAATTAC CCATGGACAC TGTTAGGTGA GGCTCATTCG GCAGCCCTGA 3900 25 AAACAAACCT GGTCACACTG TCTTTACCCT CTCCCTTCAG ATAAAGCACT TCGATTATCT 3960 ١٠. ATTGATCTGC CCAGTTTTCA AGTCATGCGA ATACTAAAAA GGTTACATCA TCTGGATCTG 4020 **30** TACCTTGGCT ATATAAGCAT GTTTTCCCCC TATTCTATGT TTCTTTTTTT GGTGAACATT 4080 GAAAAACAGG AGGTGACTTA TTACTGTTAA TTAAAACTAA ATGAAAAATG TCAAGTCTTT 4140 AAAACAGTGA GCTTGTAACT CTTTCATGTA ATTTTATTCT CTATGAATTT GGCTATCCTA 4200 Ø CTGAATCTTA AAATAAAGGA AATAAACACT TTTTTTTWAA AAAAAAGGAA AAATAMAARW 4260 M MWAAAAATCT CAATGAAATA TTTCACAAGA AGGAAAAA **4** 35 SEQ ID NO:242 PBA7 Protein sequence: H AAF91431 Protein Accession #: **40** MFTFLSSVTA AVSGLLVGYE LGIISGALLQ IKTLLALSCH EQEMVVSSLV IGALLASLTG 60 ļ.L GVLIDRYGRR TAIILSSCLL GLGSLVLILS LSYTVLIVGR IAIGVSISLS SIATCVYIAE 120 IAPOHRRGLL VSLNELMIVI GILSAYISNY AFANVFHGWK YMFGLVIPLG VLQAIAMYFL 180 PPSPRFLVMK GOEGAASKVL GRLRALSDTT EELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240 RIMIGLTLVF FVQITGQPNI LFYASTVLKS VGFQSNEAAS LASTGVGVVK VISTIPATLL 300 D 45 VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMNFTHICR SHNSINQSLD ESVIYGPGNL 360 STNNNTLRDH FKGISSHSRS SLMPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420 AFLKWLSLAS LLYYVAAFSI GLGPMPWLVL SEIFPGGIRG RAMALTSSMN WGINLISLT 480 FLTVTDLIGL PWVCFIYTIM SLDLIGLPWV CFIYTIMSLA SLLFVVMFIP ETKGCSLEQI 540 SMELAKVNYV KNNICFMSHH QEELVPKQPQ KRKPQEQLLE CNKLCGRGQS RQLSPET 50 SEQ ID NO:243 PAB4 DNA sequence: Nucleic Acid Accession#: AA172056 121-339 (underlined sequences correspond to start and stop codons) Coding sequence: 55 TTTAGCCACC AGAGGANTTC TCTTGAAATA CCCAAAATCC ATCAGTATCT TGAATCATGC 60 TGGATTTTGA AGAATTCTTA AGAAGCCATG TAAAGGGGGC TCTCTGGCCT TGAAATAGTG 120 ATGTTTTTTA TACAGAAAGG AGAATGCAGA ATGGTCAGAC TATCATGCAC TGTTAAATTT 180 GATTTCAAGA AATTACAGGA AAACTTTCCA AAGTTCCATC TCACAGAANN TTATTTINCC 240 60 AAGAATTCCA AGATAAGTTT AGTTTTATGG AAGACTTTTA TGTGGTTTTT ACTCACTCTT 300 CATCTCAGAC ATCGACAGAT GATTACATCA CITATAGTTC TAGTAAATTT ATTAATATAA 360 AACTCAGAGA CATTCCAATA TCCACATTGC TTACACCATT AGGCATAGAT TCAGTGTCAG 420 CTATGACAAT TGAAAATGAG CTGTTTTGTG ATTTAAAGGT TTAAATTTCT CTAACCAAAC 480 TGCTTGATCC AGATGCAGGA CTGCAAATGT TAATATTTGT TCTGGAAGAA CAATCAAATA 540 65 AGACTTAAGA GGAAAGGGAA TGGCCACAAT CCACCTGAAA TTTTTTCTTA AAAAGTGTGC 600 AGCCTACTAA ATCAGAATGA AAATAGAAGT ACAAGATTAT AAACAAAATG CAATCAAACT 660 TTTCTTAAGC TTACCTAAAG TTATTTCATC TGAAAATTTC AAGCAACTTT GTTCAACATT 720 AAATTGACAA TCTAAACTAA CAAGTCTTTT GAATTTATGC ATGGTAGTAA ACATTCTCC 780 TATTAACTIT ATTACCTAAG GCTAAACCTA AAATTITTAA GCAAAATTAG AAAAATAGTC 840
TTCACTCATC AAAAAATAAA GTTTGTTACA TTTAGTATTT TCCCAATAAA ATTGGTCGTT 900 70 CTTGGTTTTT TATTTGGAGA GTCTGTGCAA AATGTCACTA AAAATAAATT AGCACTAGAA 960 ATTATTTCTA AATACCAAA 75 **SEQ ID NO:244 PBQ8 DNA SEQUENCE** X51405 Nucleic Acid Accession#: Coding sequence: 3-1721 (underlined sequence corresponds to start and stop codon) 11 21 51

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AAATGGCGTG CCCGTCTCTC CGCCGGCCCC CTGCCTCGCA GTGGTTTCTC CTGCAGCTCC
           CCTGGGCTCC GCGGCCAGTA GTGCAGCCCG TGGAGCCGCG GCTTTGCCCG TCTCCTCTGG
                                                                                     120
           GTGGCCCCAG TGCGCGGGCT GACACTCATT CAGCCGGGGA AGGTGAGGCG AGTAGAGGCT
                                                                                     180
    5
           GGTGCGGAAC TTGCCGCCCC CAGCAGCGCC GGCGGGCTAA GCCCAGGGCC GGGCAGACAA
                                                                                     240
            AAGAGGCCGC CCGCGTAGGA AGGCACGGCC GGCGGCGGCG GAGCGCAGCG ATGGCCGGGC
                                                                                     300
           GAGGGGGCAG CGCGCTGCTG GCTCTGTGCG GGGCACTGGC TGCCTGCGGG TGGCTCCTGG
                                                                                     360
           GCGCCGAAGC CCAGGAGCCC GGGGCGCCCG CGGCGGCCAT GAGGCGGCGC CGGCGGCTGC
                                                                                     420
            AGCAAGAGGA CGGCATCTCC TTCGAGTACC ACCGCTACCC CGAGCTGCGC GAGGCGCTCG
                                                                                     480
   10
            TGTCCGTGTG GCTGCAGTGC ACCGCCATCA GCAGGATTTA CACGGTGGGG CGCAGCTTCG
            AGGGCCGGGA GCTCCTGGTC ATCGAGCTGT CCGACAACCC TGGCGTCCAT GAGCCTGGTG
                                                                                     600
            AGCCTGAATT TAAATACATT GGGAATATGC ATGGGAATGA GGCTGTTGGA CGAGAACTGC
                                                                                     660
            TCATTTTCTT GGCCCAGTAC CTATGCAACG AATACCAGAA GGGGAACGAG ACAATTGTCA
                                                                                     720
           ACCTGATCCA CAGTACCCGC ATTCACATCA TGCCTTCCCT GAACCCAGAT GGCTTTGAGA
                                                                                     780
   15
           AGGCAGCGTC TCAGCCTGGT GAACTCAAGG ACTGGTTTGT GGGTCGAAGC AATGCCCAGG
                                                                                     840
           GAATAGATCT GAACCGGAAC TTTCCAGACC TGGATAGGAT AGTGTACGTG AATGAGAAAG
                                                                                     900
            AAGGTGGTCC AAATAATCAT CTGTTGAAAA ATATGAAGAA AATTGTGGAT CAAAACACAA
                                                                                     960
            AGCTTGCTCC TGAGACCAAG GCTGTCATTC ATTGGATTAT GGATATTCCT TTTGTGCTTT
                                                                                    1020
           CTGCCAATCT CCATGGAGGA GACCTTGTGG CCAATTATCC ATATGATGAG ACGCGGAGTG
GTAGTGCTCA CGAATACAGC TCCTCCCCAG ATGACGCCAT TTTCCAAAGC TTGGCCCGGG
                                                                                    1080
   20
                                                                                    1140
           CATACTCTTC TTTCAACCCG GCCATGTCTG ACCCCAATCG GCCACCATGT CGCAAGAATG
                                                                                    1200
            ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTTGGTAC AGCGTACCTG
                                                                                    1260
           GAGGGATGCA AGACTTCAAT TACCTTAGCA GCAACTGTTT TGAGATCACC GTGGAGCTTA
                                                                                    1320
           GCTGTGAGAA GTTCCCACCT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAAACT
CCCTCATTAG CTACCTTGAG CAGATACACC GAGGAGTTAA AGGATTTGTC CGAGACCTTC
                                                                                    1380
₁₫25
                                                                                    1440
            AAGGTAACCC AATTGCGAAT GCCACCATCT CCGTGGAAGG AATAGACCAC GATGTTACAT
                                                                                    1500
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            CCGCAAAGGA TGGTGATTAC TGGAGATTGC TTATACCTGG AAACTATAAA CTTACAGCCT
                                                                                    1560
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            CAGCTCCAGG CTATCTGGCA ATAACAAAGA AAGTGGCAGT TCCTTACAGC CCTGCTGCTG
                                                                                    1620
           GGGTTGATTT TGAACTGGAG TCATTTTCTG AAAGGAAAGA AGAGGAGAAG GAAGAATTGA
                                                                                    1680
30
           TGGAATGGTG GAAAATGATG TCAGAAACTT TAAATTTTTA AAAAGGCTTC TAGTTAGCTG
                                                                                    1740
           CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAATGTGG TCTTTTTTTT AGATTTTGTG
                                                                                    1800
(I
           CAGTTAATAC TTAACATTGA TTTATTTTT AATCATTTAA ATATTAATCA ACTTTCCTTA
                                                                                    1860
n
            AAATAAATAG CCTCTTAGGT AAAAATATAA GAACTTGATA TATTTCATTC TCTTATATAG
                                                                                    1920
            TATTCATTTT CCTACCTATA TTACACAAAA AAGTATAGAA AAGATTTAAG TAATTTTGCC
                                                                                    1980
1 35
           ATCCTAGGCT TAAATGCAAT ATTCCTGGTA TTATTTACAA TGCAGAATTT TTTGAGTAAT TCTAGCTTTC AAAAATTAGT GAAGTTCTTT TACTGTAATT GGTGACAATG TCACATAATG
                                                                                    2040
                                                                                    2100
            AATGCTATTG AAAAGGTTAA CAGATACAGC TCGGAGTTGT GAGCACTCTA CTGCAAGACT
                                                                                    2160
            TAAATAGTTC AGTATAAATT GTCGTTTTTT TCTTGTGCTG ACTAACTATA AGCATGATCT
                                                                                    2220
□ 40
           TGTTAATGCA TTTTTGATGG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTATGAAAAG
                                                                                    2280
           AATAAAAATT GACTTCTTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG
                                                                                    2340
ļ.i.
            TTAACACTAC TTAAAAGTTT AGGGTTTTCT CTTGGTTGTA GAGTGGCCCA GAATTGCATT
            CTGAATGAAT AAAGGTTAAA AAAAAATCCC CAGTGAAAAA AAA
                             SEQ ID NO:245 PBQ8 Protein sequence
   45
           Protein Accession#:
                             P16870
           MAGRGGSALL ALCGALAACG WLLGAEAQEP GAPAAGMRRR RRLQQEDGIS FEYHRYPELR 60
           EALVSVWLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEFKYI GNMHGNEAVG 120
           RELLIFLAQY LCNEYQKGNE TIVNLIHSTR IHIMPSLNPD GFEKAASQPG ELKDWFVGRS 180
   50
           NAOGIDLNRN FPDLDRIVYV NEKEGGPNNH LLKNMKKIVD ONTKLAPETK AVIHWIMDIP 240
           FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSPDDAIFQS LARAYSSFNP AMSDPNRPPC 300
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RKNDDDSSFV DGTTNGGAWY SVPGGMQDFN YLSSNCFEIT VELSCEKFPP EETLKTYWED 360 NKNSLISYLE QIHRGVKGFV RDLQGNPIAN ATISVEGIDH DVTSAKDGDY WRLLIPGNYK 420 LTASAPGYLA ITKKVAVPYS PAAGVDFELE SFSERKEEEK EELMEWWKMM SETLNF

SEQ ID NO:246 PBY4 DNA sequence Nucleic Acid Accession#: AF038966

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60		Coung	sequence. 91-1107 (undernised sequence corresponds to start a			and stop codon)	
00	1	11	21	31	41	51	
			1	1	1	1	
	GGGGCGACGT	GAGCGCGCAG	GGGGGGGGG	GCCTCGCCTC	GTCTCTCTCT	CTGCGCCTGG	60
~ ~	GTCGGGTGGG	TGACGCCGAG	AGCCAGAGAG	ATGTCGGATT	TCGACAGTAA	CCCGTTTGCC	120
65	GACCCGGATC	TCAACAATCC	CTTCAAGGAT	CCATCAGTTA	CACAAGTGAC	AAGAAATGTT	180
	CCACCAGGAC	TTGATGAATA	TAATCCATTC	TCGGATTCTA	GAACACCTCC	ACCAGGCGGT	240
	GTGAAGATGC	CTAATGTACC	CAATACACAA	CCAGCAATAA	TGAAACCAAC	AGAGGAACAT	300
	CCAGCTTATA	CACAGATTGC	AAAGGAACAT	GCATTGGCCC	AAGCTGAACT	TCTTAAGCGC	360
~	CAAGAAGAAC	TAGAAAGAAA	AGCCGCAGAA	TTAGATCGTC	GGGAACGAGA	AATGCAAAAC	420
70	CTCAGTCAAC	ATGGTAGAAA	AAATATTTGG	CCACCTCTTC	CTAGCAATTT	TCCTGTCGGA	480
	CCTTGTTTCT	ATCAGGAATT	TTCTGTAGAC	ATTCCTGTAG	AATTCCAAAA	GACAGTAAAG	540
	CTTATGTACT	ACTTGTGGAT	GTTCCATGCA	GTAACACTGT	TTCTAAATAT	CTTCGGATGC	600
	TTGGCTTGGT	TTTGTGTTGA	TTCTGCAAGA	GCGGTTGATT	TTGGATTGAG	TATCCTGTGG	660
	TTCTTGCTTT	TTACTCCTTG	TTCATTTGTC	TGTTGGTACA	GACCACTTTA	TGGAGCTTTC	720
75	AGGAGTGACA	GTTCATTTAG	ATTCTTTGTA	TTCTTCTTCG	TCTATATTTG	TCAGTTTGCT	780
	GTACATGTAC	TCCAAGCTGC	AGGATTTCAT	AACTGGGGCA	ATTGTGGTTG	GATTTCATCC	840
	CTTACTGGTC	TCAACCAAAA	TATTCCTGTT	GGAATCATGA	TGATAATCAT	AGCAGCACTT	900
	TTCACAGCAT	CAGCAGTCAT	CTCACTAGTT	ATGTTCAAAA	AAGTACATGG	ACTATATCGC	960
00	ACAACAGGTG	CTAGTTTTGA	GAAGGCCCAA	CAGGAGTTTG	CAACAGGTGT	GATGTCCAAC	1020
δU	AAAACTGTCC	AGACCGCAGC	TGCAAATGCA	GCTTCAACTG	CAGCATCTAG	TGCAGCTCAG	1080

91-1107 (underlined sequence corresponds to start and stop codon)

	AATGCTTTCA	AGGGTAACCA	GATTTAAGAA	TCTTCAAACA	ATACACTGTT	ACCTTTTGAC	1140
	TGTACCTTTT	TCTCCAGTTA	CTGTATTCTA	CAAATATTTT	TATGTTCAAA	ACACACAGTA	1200
	CAGACAGCAT	GGATATTTCC	TGTTCACTTG	TGCATGGGCT	AAAACCAGGA	AAACTTCCTT	1260
_	GTCTTATTAC	TTTACCTAAT	AGTTTCTTAA	TATTTCAGTG	CCCCTTGCAG	AAAAAATATT	1320
5	ACATGCTAAA	TAAATATTCT	CCATATTTTT	GGGGGATGAC	ATTCAGTGAA	TTATTTCAGT	1380
	GGTGACCCAC	TGAAAATTAA	TAATGGTACT	TATGATTAAA	AACGCATTTA	ATACTAACTG	1440
	CAGTAGTTCT	TTCAAGAATC	TTTAGAGATA	AGGATTGCAC	ATTGGAAAAG	TAAACCATGT	1500
	TTCATTCCTT	TTTCCCTATT	TATATTGAAA	GAAATAGGCC	AGCAGAGACT	TAGGGATTTT	1560
10	AAATTGGCTT	GCTTTTTAGC	TGTTTCAGTC	ACCAGTGAAG	AGCCTATGTG	CATTTTGTAG	1620
10	TAGATAATGT	AAAATTTGTC	ATCTTTTTCT	TTTCTTTTTT	TTAGAATAGC	TGATATTTTG	1680
	ATAACAATCT	CTAATTTGCA	TGGGCACCAC	ATTTCTTATA	TTAAAAGAAT	TAGTGTTTTG	1740
	GCTTCTGTAC	TGCTTATGGT	TGTAGGATTC	AGGGGTTAAT	GGAATCACAG	AAATGATATT	1800
	CTGCAAGAAT	TTCTTTTAAA	TAAAAAGTTT	GGGGGTGCAA	TATAAGAAGT	TTATATAATA	1860
15	TGCAGTACAT CTTTTT	TATCCAAAAG	AGAAGGTAGT	TAATGCAGTA	GAAAGTAGTG	GTAATAATTC	1920

SEQ ID NO: 247 PBY4 Protein sequence:

Protein Accession #:

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MSDFDSNPFA DPDLNNPFKD PSVTQVTRNV PPGLDEYNPF SDSRTPPPGG VKMPNVPNTQ 60 PAIMKPTEEH PAYTQIAKEH ALAQAELLKR QEELERKAAE LDRREREMON LSOHGRKNIW 120 PPLPSNFPVG PCFYQEFSVD IPVEFQKTVK LMYYLWMFHA VTLFLNIFGC LAWFCVDSAR 180 AVDFGLSILW FLLFTPCSFV CWYRPLYGAF RSDSSFRFFV FFFVYICQFA VHVLQAAGFH 240 NWGNCGWISS LTGLNQNIPV GIMMIIIAAL FTASAVISLV MFKKVHGLYR TTGASFEKAQ 300 QEFATGVMSN KTVQTAAANA ASTAASSAAQ NAFKGNQI

SEQ ID NO:248 PBH2 DNA sequence

none found Nucleic Acid Accession#:

1-613 (underlined sequence corresponds to start and stop codon) Coding sequence:

ATGAGAGACA ATAAATCGTG TGCTTTTTTC ATGGGAAAGT TAAATGTTTG TTTTGAAGGC 60 ACAGTAATAG CAGGCTATTC AGTGTTTGCC ACTACCTGCA TCATTCATCT GGCTGTAGCT 120 AGTGCACTAC AATTTCCTAA AAAGTCTTCT CACCCTCACA GGACTGCTCT ACATCTGGCC 180 TCTGCCAATG GAAATTCAGA AGTAGTAAAA CTCCTGCTGG ACAGACGATG TCAACTTAAT 240 ATCCTTGACA ACAAAAAGAG GACAGCTCTG ACAAAGGCCG TACAATGCCA GGAAGATGAA 300 TGTGCGTTAA TGTTGCTGGA ACATGGCACT GATCCGAATA TTCCAGATGA GTATGGAAAT 360 ACCGCTCTAC ACTATGCTAT CTACAATGAA GATAAATTAA TGGCCAAAGC ACTGCTCTTA 420 TACGGTGCTG ATATCGAATC AAAAAACAAG CATGGCCTCA CACCACTGTT ACTTGGTGTA 480 CATGAGCAAA AACAGCAAGT GGTGAAATTT TTAATCAAGA AAAAAGCAAA TTTAAATGCA 540 CTGGATAGAT ATGGAAGGTG TGTGACCTTG GGAACGTTAT TTACCACCAA ATATGTTGTC 600 ATATATGAAA AGTAG

SEQ ID NO:249 PBH2 Protein sequence:

Protein Accession #:

50 MRDNKSCAFF MGKLNVCFEG TVIAGYSVFA TTCIIHLAVA SALQFPKKSS HPHRTALHLA 60 SANGNSEVVK LLLDRRCQLN ILDNKKRTAL TKAVQCQEDE CALMLLEHGT DPNIPDEYGN 120 TALHYAIYNE DKLMAKALLL YGADIESKNK HGLTPLLLGV HEQKQQVVKF LIKKKANLNA 180 LDRYGRCVTL GTLFTTKYVV IYEK

SEQ ID NO:250 PBJ1 DNA sequence Nucleic Acid Accession#: XM_005829

Coding sequence: 1-3043 (underlined sequence corresponds to start and stop codon)

60 ATGGTGATCA TCTATCTTTC TTTCTGCAAT TATTACATGG AGTTCTACAG AGAAGAGCTT 60 CCCCACATTG ACTATTTGAT TGACATTCAG TTTGCAACAG GAAAGGTTAC TCAGCCGGGA 120 GAGGACACTT CCTACCATCA ATGCGCTCAG CTTGAAGCCA GAGACGAAGG CACCGACAGT 180 TTATTATTAA ACAATGGCAG CAGCGCCACG CTGAAGACAC GAACGCGCTG TTATGGAACC 240 CCCAGAGGTC TCCCCCATCG TAGCCTGCTC CAGCCGACTC CGCCCACATG TAAAACGAAG 300 65 ATCAGGAGCA GATTTGAAGA ATTACAAAGT GAATTGGTGC CAGTCAGCAT GTCAGAGACA 360 GACCACATAG CCTCTACTTC CTCTGATAAA AATGTTGGGA AAACACCTGA ATTAAAGGAA 420 GACTCATGCA ACTTGTTTTC TGGCAATGAA AGCAGCAAAT TAGAAAATGA GTCCAAACTA 480 TTGTCATTAA ACACTGATAA AACTTTATGT CAACCTAATG AGCATAATAA TCGAATTGAA 540 GCCCAGGAAA ATTATATTCC AGATCATGGT GGAGGTGAGG ATTCTTGTGC CAAAACAGAC 600 70 ACAGGCTCAG AAAATTCTGA ACAAATAGCT AATTTTCCTA GTGGAAATTT TGCTAAACAT 660 ATTTCAAAAA CAAATGAAAC AGAACAGAAA GTAACACAAA TATTGGTGGA ATTAAGGTCA 720 TCTACATTTC CAGAATCAGC TAATGAAAAG ACTTATTCAG AAAGCCCCTA TGATACAGAC 780 TGCACCAAGA AATTTATTTC AAAAATAAAG AGCGTTTCAG CATCAGAGGA TTTGTTGGAA 840 GAAATAGAAT CTGAGCTCTT ATCTACGGAG TTTGCAGAAC ATCGAGTACC AAATGGAATG 900 75 AATAAGGGAG AACATGCATT AGTTCTGTTT GAAAAGTGTG TGCAAGATAA ATATTTGCAG 960 CAGGAACATA TCATAAAAAA GTTAATTAAA GAAAATAAGA AGCATCAGGA GCTCTTCGTA 1020 GACATTTGTT CAGAAAAAGA CAATTTAAGA GAAGAACTAA AGAAAAGAAC AGAAACTGAG 1080 AAGCAGCATA TGAACACAAT TAAACAGTTA GAATCAAGAA TAGAAGAACT TAATAAAGAA 1140 GTTAAAGCTT CCAGAGATCA ACTAATAGCT CAAGACGTTA CAGCTAAAAA TGCAGTTCAG 1200

CAGTTACACA AAGAGATGGC CCAACGGATG GAACAGGCCA ACAAGAAATG TGAAGAGGCA 1260 CGCCAAGAAA AAGAAGCAAT GGTAATGAAA TATGTAAGAG GTGAGAAGGA ATCTTTAGAT 1320 CTTCGAAAGG AAAAAGAGAC ACTTGAGAAA AAACTTAGAG ATGCAAATAA GGAACTTGAG 1380 AAAAACACTA ACAAAATTAA GCAGCTTTCT CAGGAGAAAG GACGGTTGCA CCAGCTGTAT 1440 5 GAAACTAAGG AAGGCGAAAC GACTAGACTC ATCAGAGAAA TAGACAAATT AAAGGAAGAC 1500 ATTAACTCTC ACGTCATCAA AGTAAAGTGG GCACAAAACA AATTAAAAGC TGAAATGGAT 1560 TCACACAAGG AAACCAAAGA TAAACTCAAA GAAACAACAA CAAAATTAAC ACAAGCAAAG 1620 GAAGAAGCAG ATCAGATACG AAAAAACTGT CAGGATATGA TAAAAACATA TCAGGAGTCA 1680 GAAGAAATTA AATCAAATGA GCTTGATGCA AAGCTTAGAG TCACAAAAGG AGAACTTGAA 1740 10 AAACAAATGC AAGAAAAATC TGACCAGCTA GAGATGCATC ATGCCAAAAT AAAGGAACTA 1800 GAAGATCTGA AGAGAACATT TAAGGAGGGT ATGGATGAGT TAAGAACACT GAGAACAAAG 1860 GTGAAATGTC TAGAAGATGA ACGATTAAGA ACAGAAGATG AATTATCAAA ATATAAGGAA 1920 ATTATTAATC GCCAAAAAGC TGAAATTCAG AATTTATTGG ACAAGGTGAA AACTGCAGAT 1980 CAGCTACAGG AGCAGCTTCA AAGAGGTAAG CAAGAAATTG AAAATTTGAA AGAAGAAGTG 2040 GAAAGTCTTA ATTCTTTGAT TAATGACCTA CAAAAAGACA TCGAAGGCAG TAGGAAAAGA 2100 15 GAATCTGAGC TGCTGCTGTT TACAGAAAGG CTCACTAGTA AGAATGCACA GCTTCAGTCT 2160 GAATCCAATT CTTTGCAGTC ACAATTTGAT AAAGTTTCCT GTAGTGAAAG TCAGTTACAA 2220 AGCCAGTGTG AACAAATGAA ACAGACAAAT ATTAATTTGG AAAGTAGGTT GTTGAAAGAG 2280 GAAGAACTGC GAAAAGAGGA AGTCCAAACT CTGCAAGCTG AACTCGCTTG TAGACAAACA 2340 GAAGTTAAAG CATTGAGTAC CCAGGTAGAA GAATTAAAAG ATGAGTTAGT AACTCAGAGA 2400 CGTAAACATG CCTCTAGTAT CAAGGATCTC ACCAAACAAC TTCAGCAAGC ACGAAGAAAA 2460 20 TTAGATCAGG TTGAGAGTGG AAGCTATGAC AAAGAAGTCA GCAGCATGGG AAGTCGTTCT 2520 AGTTCATCAG GGTCCCTGAA TGCTCGAAGC AGTGCAGAAG ATCGATCTCC AGAAAATACT 2580 GGGTCCTCAG TAGCTGTGGA TAACTTTCCA CAAGTAGATA AGGCCATGTT GATTGAGAGA 2640 ATAGTTAGGC TGCAAAAAGC ACATGCCCGG AAAAATGAAA AGATAGAATT TATGGAGGAC 2700 CACATCAAAC AACTGGTGGA AGAAATTAGG AAAAAAACAA AAATAATTCA AAGTTATATT 2760
TTACGAGAAG AATCAGGCAC ACTTTCTTCA GAGGCATCTG ATTTTAACAA AGTTCATTTA 2820
AGTAGACGGG GTGGCATCAT GGCATCTTTA TATACATCCC ATCCAGCTGA CAATGGATTA 2880
ACATTGGAGC TCTCTTTGGA AATCAACCGA AAATTACAGG CTGTTTTGGA GGATACGTTA 2940 J 30 CTAAAAAATA TTACTTTGAA GGAAAATCTA CAAACACTTG GAACAGAAAT AGAACGTCTT 3000 ATTAAACACC AGCATGAACT AGAACAGAGG ACAAAGAAAA CC<u>TAA</u>AACAA GCCTCTTGCT 3060 CAGTAAAGAG ACAAAAGCCA CACAGGAGTA GGTGCCACTG ACCTCTATTG TTGGAGACTT 3120 TGTTCCACTT TTTGTTTCAG CCAGTAAAAA TATTGTTTTG CTTCATCTGT ACACAAAAAA 3180 ATACCCTTTT ACAATATGAA TGCATTGCTG TATATACTGT AAGACTGAAA GCTTTGATGA 3240 **15** 35 AATTTGTTTT TGTATGGTGC AATATGACAG CCTGTCATTG AATCTAAACA ACTTAATTTG 3300 CTTGTATTCA TAAGAAGTGT TGAACATTAC AAGGGCTTTT AT E 1 SEQ ID NO:251 PBJ1 Protein sequence: **40** Protein Accession #: ļå MVIIYLSFCN YYMEFYREEL PHIDYLIDIQ FATGKVTQPG EDTSYHQCAQ LEARDEGTDS 60 T. LLLNNGSSAT LKTRTRCYGT PRGLPHRSLL QPTPPTCKTK IRSRFEELQS ELVPVSMSET 120 DHIASTSSDK NVGKTPELKE DSCNLFSGNE SSKLENESKL LSLNTDKTLC QPNEHNNRE 180
DHIASTSSDK NVGKTPELKE DSCNLFSGNE SSKLENESKL LSLNTDKTLC QPNEHNNRE 180
AQENYIPDHG GGEDSCAKTD TGSENSEQIA NFPSGNFAKH ISKTNETEGK VTQILVELRS 240
STFPESANEK TYSESPYDTD CTKKFISKIK SVSASEDLLE EIESELLSTE FAEHRVPNGM 300
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RQEKEAMYMK YVRGEKESLD LRKEKETLEK KLRDANKELE KNTNKIKQLS QEKGRLHQLY 480
ETKEGETTRL IREIDKLKED INSHVIKVKW AQNKLKAEMD SHKETKDKLK ETTTKLTQAK 540
EEADQIRKNC QDMIKTYQES EEIKSNELDA KLRVTKGELE KQMQEKSDQL EMHHAKIKEL 600 50 EDLKRTFKEG MDELRTLRTK VKCLEDERLR TEDELSKYKE IINRQKAEIQ NLLDKVKTAD 660 QLQEQLQRGK QEIENLKEEV ESLNSLINDL QKDIEGSRKR ESELLLFTER LTSKNAQLQS 720 ESNSLQSQFD KVSCSESQLQ SQCEQMKQTN INLESRLLKE EELRKEEVQT LQAELACRQT 780

SEQ ID NO:252 PBJ6 DNA sequence Nucleic Acid Accession#: D83760

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Coding sequence: 56-1459 (underlined sequence corresponds to start and stop codon)

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GAAGACCCCT CCAAACTGTG TAGACATAGT CTAAAATGTT TGGAGTGTAA TGAAGTCTTC

CAGGACGAGA CATCACTGGC TACACATTTC CAGCAGGCTG CAGATACGAG TGGACAAAAG

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		TCTGCCAGAT					2880
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		CCCACGTCAC					3000
_		GCAATGTTGT					3060
5		AAGTCTTCTA					3120
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		AGTTAAAGGA					4200
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.o		CCTTCACCTC					4560
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:F		GGAATGCTGA					5100
40		ATGGGATTTG					5160
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		CGGTAGTTCT					5580
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SEQ ID NO:255 PBJ8 Protein sequence: 55

Protein Accession #:

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SEQ ID NO:256 PBM1 DNA sequence Nucleic Acid Accession#: AF111847

Nucleic Acid Accession#: AF111847
Coding sequence: 58-1608 (underlined sequence corresponds to start and stop codon)

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						AACCTATGGA	180
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<u>25</u>						CGAGCCAGTG	1140
in made	GAGTTAAGGA	GCAGTTCTTT	CTCTAGCTGG	GATGACAGTT	CAGATTCCTA	TTGGAAAAAA	1200
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.⊒ .⊒30						GGCTGATCTG	1440
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fr						CCTGTGATTT	1800
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Ę						CCTCCTGCTC	1920
: 40							1980
<del></del> 40		AATCAGCGGA					2040
						ATTTATGTTT	2100
						GTAAATTATT	2160
i i						ACTTAAGCTT	2220
<b>45</b>						AATTGATGAG	2280
(= <b>T</b> J						ACAAATCAAT	2340 2400
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r many						GATAAGCCAA	
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		AAAAAAAAA		AAAAAAAAA	AAAAAAAA	AAAAAAAAAA	2100
	AAAAAAAAA	AAAAAAAA	MAMMAMA				
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# 70 SEQ ID NO:258 PBM4 DNA sequence Nucleic Acid Accession#: D30891 Coding sequence: 1-4032 (underlined sequence corresponds to start and stop codon)

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GACAATAATG GAAACACAGG TAATGCTACT TGCTTTGTCT TCAATGGTGG TTATATTTTC 1380 ACCTGTCGAC ATGTTGTACA TCTTATGGTG GGTAAAAACA CACATCCAAG TTTGTGGCCA 1440 GATATAATTA GCAAATGTGC GAAGGTAACC TTCACTTATA CAGAGTTCTG CCCTACTCCT 1500 GACAATTGGT TTTCCATTGA GCCATGGCTT AAAGTGTCCA ATGAAAATCT AGATTATGCC 1560 20 ATTTTAAAAC TAAAAGAAAA TGGAAATGCG TTTCCTCCAG GACTATGGCG ACAGATTTCT 1620 CCTCAACCAT CTACTGGTTT GATTTATTTA ATTGGTCATC CTGAAGGCCA GATCAAGAAA 1680 ATAGATGGTT GTACTGTGAT TCCTCTAAAC GAACGATTGA AAAAATATCC AAACGATTGT 1740 CAAGATGGGT TGGTAGATCT CTATGATACC ACCAGTAATG TATACTGTAT GTTTACCCAA 1800 AGAAGTTTCC TATCAGAGGT TTGGAACACA CACACGCTTA GTTATGATAC TTGTTTCTCT 1860 **25** GATGGGTCCT CAGGCTCCCC AGTGTTTAAT GCATCTGGCA AATTGGTTGC TTTGCATACC 1920 TTTGGGCTTT TTTATCAACG AGGATTTAAT GTGCATGCCC TTATTGAATT TGGTTATTCT 1980 ij ATGGATTCTA TTCTTTGTGA TATTAAAAAG ACAAATGAGA GCTTGTATAA ATCATTAAAT 2040 GATGAGAAAC TTGAGACCTA CGATGAAGAG AAAGCCCGGC CCAGGCCAGC CTACCGGCGA 2100 CTAGGATGCT TTCGCTTTCG CTCTCGCTTT CCAATACTCG GGACTGGGGA AACCGGGAGA 2160 ATAGAAGCAG GCAAGGACCG CCGTGGGCAC GGGGTCAGTG AGACAGGGTC CTGCTCGCGG 2220 M CGTCAAGGAG GAGCGCTGTG GGTGTCCCCA GCGCAGCCAA TCGGCTTCCG AAGTAGCTGG 2280 AGCTCTGGAG CCTTTGCTTC CTCAAATACG AGCGGGAACT GCGTTGAGCG CTGGATTCCA 2340 Ø GGCCGAGTGC TGGCGAGGCG CGCAGTCTCT AAAGAGCAAC AGAATAATTG CAGTACTTCT 2400 CTAATGAGGA TGGAGTCTAG AGGAGACCCA AGAGCCACAA CTAATACCCA GGCTCAAAGA 2460 TTCCATTCAC CTAAGAAAAA TCCAGAAGAC CAGACCATGC CCCAAAATAG GACAATATAT 2520 GTTACCTTGA AGGCTGTCAG AAAAGAGATA GAAACTCACC AAGGCCAAGA AATGCTTGTG 2580 CGTGGCACAG AAGGAATCAA AGAGTACATA AACCTTGGAA TGCCCCTCAG TTGTTTCCCT 2640 GAAGGTGGCC AGGTGGTCAT TACATTTTCC CAAAGTAAAA GTAAGCAGAA GGAAGATAAC 2700 CACATATTTG GCAGGCAGGA CAAAGCATCG ACTGAATGTG TCAAATTTTA CATTCATGCA 2760 40 45 ATTGGAATTG GGAAGTGTAA AAGAAGGATT GTTAAATGTG GGAAGCTTCA CAAAAAGGGG 2820 CGCAAACTCT GTGTTTATGC TTTCAAAGGA GAAACCATCA AGGATGCACT GTGCAAGGAT 2880 GGCAGATTTC TTTCCTTTCT GGAGAATGAT GATTGGAAAA TCATTGAAAA CAATGACACC 2940 ATTTTAGAAA GCACCCAGCC AGTTGATGAA TTAGAAGGCA 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#### 10 SEQ ID NO:259 PBM4 Protein sequence: PBM4 Protein sequence: BAB67788

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LKCLPSDSHF KITFGQRKSS KEDGHILRQC ENPNMECILF HVVAIGRTRK KIVKINELHE 180

KGSKLCIYAL KGETIEGALC KDGRFRSDIG EFEWKLKEGH KKIYGKQSMV DEVSGKVLEM 240

DISKKKALQQ KDIHKKIKQN ESATDEINHQ SLIQSKKKVH KPKKDGETKD VEHSREQILP 300

PQDLSHYIKD KTRQTIPRIR NYYFCSLPRK YRQINSQVRR RPHLGRRYAI NLDVQKEAIN 360

LLKNYQTLNE AIMHQYPNFK EEAQWVRKYF REEQKRMNLS PAKQFNIYKK DFGKMTANSV 420 15 20 SVATCEQLTY YSKSVGFMQW DNNGNTGNAT CFVFNGGYIF TCRHVVHLMV GKNTHPSLWP 480 DIISKCAKVT FTYTEFCPTP DNWFSIEPWL KVSNENLDYA ILKLKENGNA FPPGLWRQIS 540 PIPSTCARVI F11 TEPC-17 DINWFSIEPWE KVSNENEJTA IEREKENONA FFOLDWQIS 340
POPSTGLIYL IGHPEGQIKK IDGCTVIPLN ERLKKYPNDC QDGLVDLYDT TSNVYCMFTQ 600
RSFLSEVWNT HTLSYDTCFS DGSSGSPVFN ASGKLVALHT FGLFYQRGFN VHALIEFGYS 660
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IEAGKDRRGH GVSETGSCSR RQGGALWVSP AQPIGFRSSW SSGAFASSNT SGNCVERWIP 780
GRVLARRAVS KEQQNNCSTS LMRMESRGDP RATTNTQAQR FHSPKKNPED QTMPQNRTIY 840 __25 VTLKAVRKEI ETHOGOEMLV RGTEGIKEYI NLGMPLSCFP EGGQVVITFS QSKSKQKEDN 900 HIFGRQDKAS TECVKFYIHA IGIGKCKRRI VKCGKLHKKG RKLCVYAFKG ETIKDALCKD 960 TCVLREQIVA QYPSLKRESE KIIENFKKKM KVKNGETLFE LHRTTFGKVT KNSSSIKVVK 1080 LLVRLSDSVG YLFWDSATTG YATCFVFKGL FILTCRHVID SIVGDGIEPS KWATIIGQCV 1140 RVTFGYEELK DKETNYFFVE PWFEIHNEEL DYAVLKLKEN GQQVPMELYN GITPVPLSGL 1200 IHIIGHPYGE KKQIDACAVI PQGQRAKKCQ ERVQSKKAES PEYVHMYTQR SFQKIVHNPD 1260 -30 M Ø VITYDTEFFF GASGSPVFDS KGSLVAMHAA GFAYTYQNET RSIIEFGSTM ESILLDIKQR 1320 35 HKPWYEEVFV NQQDVEMMSD EDL Ø

## SEQ ID NO:260 PBQ1 DNA sequence Nucleic Acid Accession#: NM_015642

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489-2489 (underlined sequence corresponds to start and stop codon) Coding sequence:

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2280

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           2700
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                                                                                    2820
           ΔΑΔΑΔΑΔΔ
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          QPRPVRIQTL VGNIHIKQEM EDDYDYYGQQ RVQILERNES EECTEDTDQA EGTESEPKGE 300
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TSNTQVIGTA GNTYLPALFT TQPAGSGPKP FLFSLPQPLA GQQTQFVTVS QPGLSTFTAQ 480
LPAPQPLASS AGHSTASGQG EKKPYECTLC NKTFTAKQNY VKHMFVHTGE KPHQCSICWR 540
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          MRMHVSDG
- 30
m
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          Nucleic Acid Accession#: AI654187
                             1-912 (underlined sequence corresponds to start and stop codon)
          Codina sequence:
35
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                                                           41
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45
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                                                                                     540
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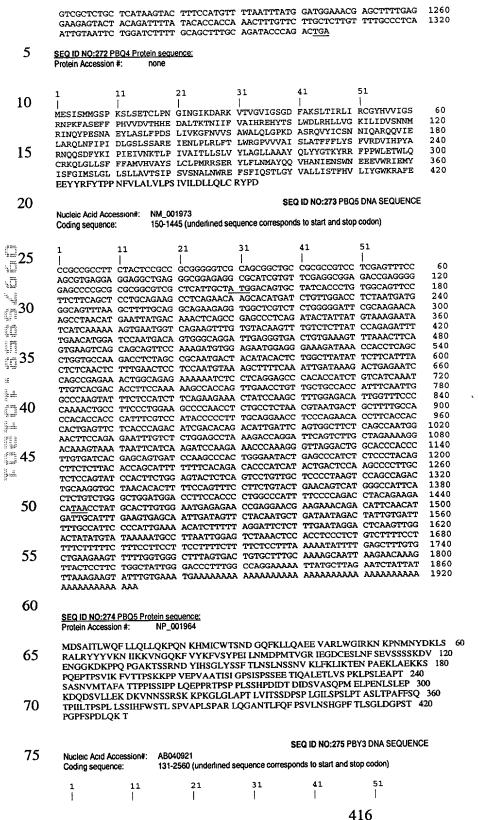
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Attorney Docket No.: 018501-004200US

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SEQ ID NO:277 PBY6 DNA SEQUENCE

Nucleic Acid Accession#: AA464018 75 Coding sequence: 64-1669(underlined sequence corresponds to start and stop codon)

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AAGAAGCTGC GGAGCATTGA GGTGCTACAG AAGGTGCTGT GTGCCGCACA GGAACGCTCC 960
CGGCTCACGT ACGCCCAGCA CCAGGAGGAG GATGACCTGC TGAACCTGAT CGACGCCCCC 1020 15 AGTGTTGTTG CTAAAACTGA GCAAGAGGTT GACATTATAT TGCCCCAGTT CTCCAAGCTG 1080 ACAGTCACGG ACTTCTTCCA GAAGCTGGGC CCCTTATCTG TGTTTTCGGC TAACAAGCGG 1140 TGGACGCCTC CTCGAAGCAT CCGCTTCACT GCAGAAGAAG GGGACTTGGG GTTCACCTTG 1200 AGAGGGAACG CCCCGTTCA GGTTCACTTC CTGGATCCTT ACTGCTCTGC CTCGGTGGCA 1260 GGAGCCCGGG AAGGAGATTA TATTGTCTCC ATTCAGCTTG TGGATTGTAA GTGGCTGACG 1320 CTGAGTGAGG TTATGAAGCT GCTGAAGAGC TTTGGCGAGG ACGAGATCGA GATGAAAGTC 1380 20 GTGAGCCTCC TGGACTCCAC ATCATCCATG CATAATAAGA GTGCCACATA CTCCGTGGGA 1440 ATGCAGAAAA CGTACTCCAT GATCTGCTTA GCCATTGATG ATGACGACAA AACTGATAAA 1500 ACCAAGAAA TCTCCAAGAA GCTTTCCTTC CTGAGTTGGG GCACCAACAA GAACAGACAG 1560 25 AAGTCAGCCA GCACCTTGTG CCTCCCATCG GTCGGGGCTG CACGGCCTCA GGTCAAGAAG 1620 AAGCTGCCCT CCCCTTTCAG CCTTCTCAAC TCAGACAGTT CTTGGTACTA A

### SEQ ID NO:278 PBY6 Protein sequence: Protein Accession #:

Nucleic Acid Accession#: AF107493

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DFILEHYSED GYLYEDEIAD LMDLRQACRT PSRDEAGVEL LMTYFIQLGF VESRFFPPTR 60 QMGLLFTWYD SLTGVPVSQQ NLLLEKASVL FNTGALYTQI GTRCDRQTQA GLESAIDAFQ 120 RAAGVLNYLK DTFTHTPSYD MSPAMLSVLV KMMLAQAQES VFEKISLPGI RNEFFMLVKV 180 AQEAAKVGEV YQQLHAAMSQ APVKENIPYS WASLACVKAH HYAALAHYFT AILLIDHQVK 240 PGTDLDHQEK CLSQLYDHMP EGLTPLATLK NDQQRRQLGK SHLRRAMAHH EESVREASLC 300 KKLRSIEVLQ KVLCAAQERS RLTYAQHQEE DDLLNLIDAP SVVAKTEQEV DIILPQFSKL 360 TVTDFFQKLG PLSVFSANKR WTPPRSIRFT AEEGDLGFTL RGNAPVQVHF LDPYCSASVA 420 GAREGDYIVS IOLVDCKWLT LSEVMKLLKS FGEDEIEMKV VSLLDSTSSM HNKSATYSVG 480 MQKTYSMICL AIDDDDKTDK TKKISKKLSF LSWGTNKNRQ KSASTLCLPS VGAARPQVKK 540 KLPSPFSLLN SDSSWY

### SEQ ID NO:279 PBY8 DNA SEQUENCE

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泽			GCACATCGTG				420
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           Protein Accession #:
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                                                                                360
          SRVMDLKGQM IYIVESSAIL FLGSPCVDRL EDFTGRGLYL SDIPIHNALR DVVLIGEQAR
                                                                                420
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VTLANKFESC SVPRKINVSP TTYRLLKDCP GFVFTPRSRE ELPPNFPSEI PGICHFLDAY OOGTNSKPCF OKKDVEDGNA NFLGKASGID 5 SEQ ID NO:287 PFD2 DNA SEQUENCE Nucleic Acid Accession#: NM_000720 119-6664 (underlined sequence corresponds to start and stop codon) Coding sequence: 10 11 21 31 AGAATAAGGG CAGGGACCGC GGCTCCTATC TCTTGGTGAT CCCCTTCCCC ATTCCGCCCC 60 CGCCTCAACG CCCAGCACAG TGCCCTGCAC ACAGTAGTCG CTCAATAAAT GTTCGTGGAT 120 15 GATGATGATG ATGATGA AAAAAATGCA GCATCAACGG CAGCAGCAAG CGGACCACGC 180 GAACGAGGCA AACTATGCAA GAGGCACCAG ACTTCCTCTT TCTGGTGAAG GACCAACTTC 240 TCAGCCGAAT AGCTCCAAGC AAACTGTCCT GTCTTGGCAA GCTGCAATCG ATGCTGCTAG ACAGGCCAAG GCTGCCCAAA CTATGAGCAC CTCTGCACCC CCACCTGTAG GATCTCTCTC CCAAAGAAAA CGTCAGCAAT ACGCCAAGAG CAAAAAACAG GGTAACTCGT CCAACAGCCG 420 20 ACCTGCCCGC GCCCTTTTCT GTTTATCACT CAATAACCCC ATCCGAAGAG CCTGCATTAG 480 TATAGTGGAA TGGAAACCAT TTGACATATT TATATTATTG GCTATTTTTG CCAATTGTGT 540 GGCCTTAGCT ATTTACATCC CATTCCCTGA AGATGATTCT AATTCAACAA ATCATAACTT GGAAAAAGTA GAATATGCCT TCCTGATTAT TTTTACAGTC GAGACATTTT TGAAGATTAT 660 <u>√</u>25 AGCGTATGGA TTATTGCTAC ATCCTAATGC TTATGTTAGG AATGGATGGA ATTTACTGGA 720 TTTTGTTATA GTAATAGTAG GATTGTTTAG TGTAATTTTG GAACAATTAA CCAAAGAAAC 780 AGAAGGCGGG AACCACTCAA GCGGCAAATC TGGAGGCTTT GATGTCAAAG CCCTCCGTGC 840 Ū CTTTCGAGTG TTGCGACCAC TTCGACTAGT GTCAGGGGTG CCCAGTTTAC AAGTTGTCCT 900 GAACTCCATT ATAAAAGCCA TGGTTCCCCT CCTTCACATA GCCCTTTTGG TATTATTTGT 960 AATCATAATC TATGCTATTA TAGGATTGGA ACTTTTTATT GGAAAAATGC ACAAAACATG 1020 30 TTTTTTGCT GACTCAGATA TCGTAGCTGA AGAGGACCCA GCTCCATGTG CGTTCTCAGG 1080 GAATGGACGC CAGTGTACTG CCAATGGCAC GGAATGTAGG AGTGGCTGGG TTGGCCCGAA 1140 m CGGAGGCATC ACCAACTITG ATAACTITGC CTTTGCCATG CTTACTGTGT TTCAGTGCAT 1200 CACCATGGAG GGCTGGACAG ACGTGCTCTA CTGGGTAAAT GATGCGATAG GATGGGAATG 1260 O GCCATGGGTG TATTTTGTTA GTCTGATCAT CCTTGGCTCA TTTTTCGTCC TTAACCTGGT 1320 35 TCTTGGTGTC CTTAGTGGAG AATTCTCAAA GGAAAGAGAG AAGGCAAAAG CACGGGGAGA 1380 TTTCCAGAAG CTCCGGGAGA AGCAGCAGCT GGAGGAGGAT CTAAAGGGCT ACTTGGATTG 1440 ű GATCACCCAA GCTGAGGACA TCGATCCGGA GAATGAGGAA GAAGGAGGAG AGGAAGGCAA ACGAAATACT AGCATGCCCA CCAGCGAGAC TGAGTCTGTG AACACAGAGA ACGTCAGCGG 1560 :5 TGAAGGCGAG AACCGAGGCT GCTGTGGAAG TCTCTGGTGCTGGAGAC GGAGAGGGGGC 1620 **40** GGCCAAGGCG GGGCCCTCTG GGTGTCGGCG GTGGGGTCAA GCCATCTCAA AATCCAAACT 1680 CAGCCGACGC TGGCGTCGCT GGAACCGATT CAATCGCAGA AGATGTAGGG CCGCCGTGAA 1740 GTCTGTCACG TTTTACTGGC TGGTTATCGT CCTGGTGTTT CTGAACACCT TAACCATTTC 1800 CTCTGAGCAC TACAATCAGC CAGATTGGTT GACACAGATT CAAGATATTG CCAACAAAGT 1860 CCTCTTGGCT CTGTTCACCT GCGAGATGCT GGTAAAAATG TACAGCTTGG GCCTCCAAGC 1920 45 ATATTTCGTC TCTCTTTTCA ACCGGTTTGA TTGCTTCGTC GTGTGTGGTG GAATCACTGA GACGATCCTG GTGGAACTGG AAATCATGTC TCCCCTGGGG ATCTCTGTGT TTCGGTGTGT 1980 2040 12 GCGCCTCTTA AGAATCTTCA AAGTGACCAG GCACTGGACT TCCCTGAGCA ACTTAGTGGC 2100 i d ATCCTTATTA AACTCCATGA AGTCCATCGC TTCGCTGTTG CTTCTGCTTT TTCTCTTCAT 2160 TATCATCTTT TCCTTGCTTG GGATGCAGCT GTTTGGCGGC AAGTTTAATT TTGATGAAAC 2220 50 GCAAACCAAG CGGAGCACCT TTGACAATTT CCCTCAAGCA CTTCTCACAG TGTTCCAGAT 2280 CCTGACAGGC GAAGACTGGA ATGCTGTGAT GTACGATGGC ATCATGGCTT ACGGGGGCCC 2340 ATCCTCTTCA GGAATGATCG TCTGCATCTA CTTCATCATC CTCTTCATTT GTGGTAACTA 2400 TATTCTACTG AATGTCTTCT TGGCCATCGC TGTAGACAAT TTGGCTGATG CTGAAAGTCT 2460 GAACACTGCT CAGAAAGAAG AAGCGGAAGA AAAGGAGAGG AAAAAGATTG CCAGAAAAGA 2520 55 GAGCCTAGAA AATAAAAAGA ACAACAAACC AGAAGTCAAC CAGATAGCCA ACAGTGACAA 2580 CAAGGTTACA ATTGATGACT ATAGAGAAGA GGATGAAGAC AAGGACCCCT ATCCGCCTTG 2640 CGATGTGCCA GTAGGGGAAG AGGAAGAGGA AGAGGAGGAG GATGAACCTG AGGTTCCTGC 2700 CGGACCCCGT CCTCGAAGGA TCTCGGAGTT GAACATGAAG GAAAAAATTG CCCCCATCCC 2760 TGAAGGGAGC GCTTTCTTCA TTCTTAGCAA GACCAACCCG ATCCGCGTAG GCTGCCACAA 2820 60 GCTCATCAAC CACCACATCT TCACCAACCT CATCCTTGTC TTCATCATGC TGAGCAGCGC 2880 TGCCCTGGCC GCAGAGGACC CCATCCGCAG CCACTCCTTC CGGAACACGA TACTGGGTTA 2940 CTTTGACTAT GCCTTCACAG CCATCTTTAC TGTTGAGATC CTGTTGAAGA TGACAACTTT 3000 TGGAGCTTTC CTCCACAAAG GGGCCTTCTG CAGGAACTAC TTCAATTTGC TGGATATGCT 3060 GGTGGTTGGG GTGTCTCTGG TGTCATTTGG GATTCAATCC AGTGCCATCT CCGTTGTGAA 65 GATTCTGAGG GTCTTAAGGG TCCTGCGTCC CCTCAGGGCC ATCAACAGAG CAAAAGGACT
TAAGCACGTG GTCCAGTGCG TCTTCGTGGC CATCCGGACC ATCGGCAACA TCATGATCGT 3180 3240 CACTACCCTC CTGCAGTTCA TGTTTGCCTG TATCGGGGTC CAGTTGTTCA AGGGGAAGTT 3300 CTATCGCTGT ACGGATGAAG CCAAAAGTAA CCCTGAAGAA TGCAGGGGAC TTTTCATCCT 3360 CTACAAGGAT GGGGATGTTG ACAGTCCTGT GGTCCGTGAA CGGATCTGGC AAAACAGTGA 3420 70 TTTCAACTTC GACAACGTCC TCTCTGCTAT GATGGCGCTC TTCACAGTCT CCACGTTTGA 3480 GGGCTGGCCT GCGTTGCTGT ATAAAGCCAT CGACTCGAAT GGAGAGAACA TCGGCCCAAT 3540 CTACAACCAC CGCGTGGAGA TCTCCATCTT CTTCATCATC TACATCATCA TTGTAGCTTT 3600 CTTCATGATG AACATCTTTG TGGGCTTTGT CATCGTTACA TTTCAGGAAC AAGGAGAAAA 3660 AGAGTATAAG AACTGTGAGC TGGACAAAAA TCAGCGTCAG TGTGTTGAAT ACGCCTTGAA AGCACGTCCC TTGCGGAGAT ACATCCCCAA AAACCCCTAC CAGTACAAGT TCTGGTACGT 3720 75 3780 GGTGAACTCT TCGCCTTTCG AATACATGAT GTTTGTCCTC ATCATGCTCA ACACACTCTG 3840 CTTGGCCATG CAGCACTACG AGCAGTCCAA GATGTTCAAT GATGCCATGG ACATTCTGAA 3900 CATGGTCTTC ACCGGGGTGT TCACCGTCGA GATGGTTTTG AAAGTCATCG CATTTAAGCC 3960 TAAGGGGTAT TTTAGTGACG CCTGGAACAC GTTTGACTCC CTCATCGTAA TCGGCAGCAT 4020 80 TATAGACGTG GCCCTCAGCG AAGCGGACCC AACTGAAAGT GAAAATGTCC CTGTCCCAAC

ESDTHAVQIA LMALKMMELS DEVMSPHGEP IKMRIGLHSG SVFAGVVGVK MPRYCLFGNN

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                                                                               5940
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  75
          ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
          CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAAT ACAAGGGGAC 1320
```

GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCCATGCC

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It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.